GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: December 21, 2001, 19:24:31 ; Search time 796.8 Seconds
(without alignments)
18.291 Million cell updates/sec

Title: US-09-554-267-3
Perfect score: 17
Sequence: 1 ggcccccatggtggagg 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 989696

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_1101:*
1: /SIDS2/gcgdata/geneseq/geneseqn/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	17	100.0	18	15	AAQ77634	Ribonucleotide to
c	2	17	100.0	18	15	AAQ77620	Antisense polynucl
c	3	17	100.0	18	15	AAQ77648	Antisense ribonucl
	4	17	100.0	18	15	AAQ76393	Polynucleotide to
c	5	17	100.0	36	15	AAQ76387	Tenascin gene cons
	6	17	100.0	36	15	AAQ76386	Tenascin gene cons
c	7	17	100.0	36	15	AAQ77661	Tenascin gene mRNA
	8	17	100.0	36	15	AAQ77662	Tenascin gene mRNA
c	9	15.4	90.6	33	21	AAA30431	Human ACAM#6 cDNA
c	10	15.4	90.6	33	21	AAA30437	Human ACAM#4 cDNA
	11	15	88.2	24	15	AAQ77617	Polynucleotide to
c	12	15	88.2	24	15	AAQ77659	Antisense ribonucl
c	13	15	88.2	24	15	AAQ77631	Antisense polynucl
	14	15	88.2	24	15	AAQ77645	Ribonucleotide to
	15	14.4	84.7	34	19	AAV68229	Human cytostatin I
c	16	14.4	84.7	35	20	AAZ33020	Human ATR-5 L chai
c	17	14.4	84.7	35	22	AAF87845	ATR-5 L chain V re
c	18	14	82.4	34	17	AAT10560	Serum paraoxonase
c	19	13.8	81.2	31	21	AAZ58151	Human FAST-1 gene
c	20	13.8	81.2	41	18	AAT97210	Kappa chain variab
c	21	13.8	81.2	46	21	AAA75783	PCR primer for a h
c	22	13.4	78.8	24	21	AAZ61427	PCR primer for DNA
c	23	13.4	78.8	27	18	AAT90893	5' primer for epid
	24	13.4	78.8	27	20	AAX88424	IBV M protein PCR
c	25	13.4	78.8	31	18	AAT68725	Human osteo antivi
c	26	13.4	78.8	31	19	AAV45332	Human extracellula
c	27	13.4	78.8	32	17	AAT39712	Ubiquitin conjugat
c	28	13.4	78.8	32	18	AAT79829	Primer used for am
c	29	13.4	78.8	32	20	AAZ25321	Human ubiquitin co
c	30	13.4	78.8	32	20	AAV82882	5' PCR primer used
c	31	13.4	78.8	33	17	AAT39706	Ubiquitin conjugat
c	32	13.4	78.8	33	18	AAT79823	Primer used for am
c	33	13.4	78.8	33	20	AAZ25315	Human ubiquitin co
c	34	13.4	78.8	33	20	AAV82876	5' PCR primer used
c	35	13.4	78.8	35	20	AAX36573	PCR primer for hum
c	36	13.4	78.8	35	22	AAS00262	LPA receptor-relat
c	37	13.4	78.8	36	21	AAA74814	Human erythropoiet
c	38	13.4	78.8	43	17	AAT42077	Human erythropoiet
c	39	13.4	78.8	43	21	AAC60363	Primer EPO-START.
c	40	13.4	78.8	43	22	AAF80219	PCR primer used to
c	41	13.4	78.8	47	15	AAQ68640	A33 heavy chain va
c	42	13.4	78.8	47	16	AAQ80383	Mouse light chain
c	43	13.4	78.8	47	16	AAQ80450	L243 VL region 5'
c	44	13	76.5	24	16	AAQ80830	Lipopolysaccharide
c	45	13	76.5	24	19	AAV10334	Human rLBP PCR pri

ALIGNMENTS

RESULT 1
AAQ77634
ID AAQ77634 standard; RNA; 18 BP.
XX
AC AAQ77634;
XX
DT 02-JUN-1995 (first entry)
XX
DE Ribonucleotide to tenascin gene consensus mRNA initiation site -9-+9.
XX
KW Antisense; polynucleotide; sense strand; tenascin; complementary;
KW consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW proliferation; growth stimulatory; transcription; vascular stenosis;
KW post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW organ transplant; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_difference 1..18
FT /*tag= a
FT /note= "phosphodiester bonds between nucleotides
FT may be replaced by phosphorothioate bonds"
XX
PN WO9421664-A.
XX
PD 29-SEP-1994.
XX
PF 24-MAR-1994; 94WO-US03206.
XX
PR 25-MAR-1993; 93US-0037025.
XX
PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX

PI Denner LA, Dixon RAF, Rege AA, Stacy DL;
XX
DR WPI; 1994-316926/39.
XX
PT Synthetic anti-sense polynucleotide - hybridises to tenascin
PT gene, useful for inhibiting vascular smooth muscle cell
PT proliferation.
XX
PS Claim 5; Page 47; 64pp; English.
XX
CC A series of polynucleotides, either DNA (AAQ76388 and AAQ76392-400 and
CC AAQ77614-18) or RNA (AAQ76390 and AAQ77633-46), directed against the
CC consensus mRNA initiation site sequence (AAQ77661) for the tenascin gene.
CC The polynucleotides are based on the degenerate sequence (AAQ76386) of
CC the tenascin gene. Tenascin is an extracellular matrix glycoprotein
CC consisting six disulphide-linked subunits, each having molecular mass of
CC 190-250 kDa. Tenascin may be important for smooth muscle cell
CC proliferation as the protein has growth stimulatory activity. The
CC polynucleotides can be used to inhibit transcription of the gene or
CC translation of the mRNA encoding tenascin. The method is applicable to a
CC number of diseases where the proliferation of smooth muscle is involved
CC e.g. vascular stenosis, post-angioplasty restenosis and other
CC non-angioplasty procedures such as cardiac hypertrophy, vascular surgery
CC and organ transplant.
XX
SQ Sequence 18 BP; 2 A; 5 C; 8 G; 3 U; 0 other;

Query Match 100.0%; Score 17; DB 15; Length 18;
Best Local Similarity 88.2%; Pred. No. 18;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ggccccccatggtggagg 17
||||||||:||:|||||
Db 1 ggcccccaugguggagg 17

RESULT 2
AAQ77620/c
ID AAQ77620 standard; DNA; 18 BP.
XX
AC AAQ77620;
XX
DT 01-JUN-1995 (first entry)
XX
DE Antisense polynucleotide binds to tenascin gene consensus at -9-+9.
XX
KW Antisense; polynucleotide; sense strand; tenascin; complementary;
KW consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW proliferation; growth stimulatory; transcription; vascular stenosis;
KW post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW organ transplant; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_difference 1..18
FT /*tag= a
FT /note= "phosphodiester bonds between nucleotides
FT may be replaced by phosphorothioate bonds"
XX
PN WO9421664-A.
XX
PD 29-SEP-1994.
XX
PF 24-MAR-1994; 94WO-US03206.
XX
PR 25-MAR-1993; 93US-0037025.
XX
PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI Denner LA, Dixon RAF, Rege AA, Stacy DL;
XX
DR WPI; 1994-316926/39.
XX
PT Synthetic anti-sense polynucleotide - hybridises to tenascin
PT gene, useful for inhibiting vascular smooth muscle cell
PT proliferation.
XX
PS Claim 10; Page 44; 64pp; English.
XX
CC A series of antisense polynucleotides, either DNA (AAQ76388 and
CC AAQ77619-32) or RNA (AAQ76390 and AAQ77647-60) directed against the sense
CC strand of the gene encoding tenascin. The polynucleotides are based on
CC the complementary sequence (AAQ76386) of the consensus mRNA initiation
CC site sequence (AAQ77661) for the tenascin gene. Tenascin is an
CC extracellular matrix glycoprotein consisting six disulphide-linked
CC subunits, each having molecular mass of 190-250 kDa. Tenascin may be
CC important for smooth muscle cell proliferation as the protein has growth
CC stimulatory activity. The polynucleotides can be used to inhibit
CC transcription of the gene or translation of the mRNA encoding tenascin.
CC The method is applicable to a number of diseases where the proliferation
CC of smooth muscle is involved e.g. vascular stenosis, post-angioplasty
CC restenosis and other non-angioplasty procedures such as cardiac
CC hypertrophy, vascular surgery and organ transplant.
XX
SQ Sequence 18 BP; 3 A; 8 C; 5 G; 2 T; 0 other;

Query Match 100.0%; Score 17; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ggccccccatggtggagg 17
||||||||||||||||||
Db 18 GGCCCCCATGGTGGAGG 2

RESULT 3
AAQ77648/c
ID AAQ77648 standard; RNA; 18 BP.
XX
AC AAQ77648;
XX
DT 02-JUN-1995 (first entry)
XX
DE Antisense ribonucleotide binds to tenascin gene consensus at -9-+9.
XX
KW Antisense; polynucleotide; sense strand; tenascin; complementary;
KW consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW proliferation; growth stimulatory; transcription; vascular stenosis;
KW post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW organ transplant; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_difference 1..18
FT /*tag= a
FT /note= "phosphodiester bonds between nucleotides
FT may be replaced by phosphorothioate bonds"
XX
PN WO9421664-A.
XX
PD 29-SEP-1994.
XX
PF 24-MAR-1994; 94WO-US03206.
XX
PR 25-MAR-1993; 93US-0037025.
XX
PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI Denner LA, Dixon RAF, Rege AA, Stacy DL;
XX
DR WPI; 1994-316926/39.
XX

```
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 10; Page 51; 64pp; English.
XX
CC   A series of antisense polynucleotides, either DNA (AAQ76388 and
CC   AAQ77619-32) or RNA (AAQ76390 and AAQ77647-60) directed against the sense
CC   strand of the gene encoding tenascin.  The polynucleotides are based on
CC   the complementary sequence (AAQ76386) of the consensus mRNA initiation
CC   site sequence (AAQ77661) for the tenascin gene.  Tenascin is an
CC   extracellular matrix glycoprotein consisting six disulphide-linked
CC   subunits, each having molecular mass of 190-250 kDa.  Tenascin may be
CC   important for smooth muscle cell proliferation as the protein has growth
CC   stimulatory activity.  The polynucleotides can be used to inhibit
CC   transcription of the gene or translation of the mRNA encoding tenascin.
CC   The method is applicable to a number of diseases where the proliferation
CC   of smooth muscle is involved e.g. vascular stenosis, post-angioplasty
CC   restenosis and other non-angioplasty procedures such as cardiac
CC   hypertrophy, vascular surgery and organ transplant.
XX
SQ   Sequence 18 BP; 3 A; 8 C; 5 G; 2 U; 0 other;

  Query Match             100.0%;  Score 17;  DB 15;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 18;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggccccccatggtggagg 17
          |||||||||||||||||
Db     18 GGCCCCCCATGGTGGAGG 2


RESULT   4
AAQ76393
ID   AAQ76393 standard; DNA; 18 BP.
XX
AC   AAQ76393;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Polynucleotide to tenascin gene consensus mRNA initiation site -9-+9.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..18
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                          may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 5; Page 40; 64pp; English.
XX
CC   A series of polynucleotides, either DNA (AAQ76388 and AAQ76392-400 and
CC   AAQ77614-18) or RNA (AAQ76390 and AAQ77633-46), directed against the
CC   consensus mRNA initiation site sequence (AAQ77661) for the tenascin gene.
CC    The polynucleotides are based on the degenerate sequence (AAQ76386) of
CC   the tenascin gene.  Tenascin is an extracellular matrix glycoprotein
CC   consisting six disulphide-linked subunits, each having molecular mass of
CC   190-250 kDa.  Tenascin may be important for smooth muscle cell
CC   proliferation as the protein has growth stimulatory activity.  The
CC   polynucleotides can be used to inhibit transcription of the gene or
CC   translation of the mRNA encoding tenascin. The method is applicable to a
CC   number of diseases where the proliferation of smooth muscle is involved
CC   e.g. vascular stenosis, post-angioplasty restenosis and other
CC   non-angioplasty procedures such as cardiac hypertrophy, vascular surgery
CC   and organ transplant.
XX
SQ   Sequence 18 BP; 2 A; 5 C; 8 G; 3 T; 0 other;

  Query Match             100.0%;  Score 17;  DB 15;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 18;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggccccccatggtggagg 17
          |||||||||||||||||
Db      1 ggccccccatggtggagg 17


RESULT   5
AAQ76387/c
ID   AAQ76387 standard; DNA; 36 BP.
XX
AC   AAQ76387;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Tenascin gene consensus DNA sequence sense strand.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..36
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                          may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
```

```
PS   Claim 6; Page 39; 64pp; English.
XX
CC   A series of polynucleotides, either DNA (AAQ76389 and AAQ76392-400 and
CC   AAQ77614-18) or RNA (AAQ76391 and AAQ77633-46), directed against the
CC   consensus mRNA initiation site sequence (AAQ77661) for the tenascin gene.
CC    The polynucleotides are based on the sense strand sequence (AAQ76387) of
CC   the tenascin gene.  Tenascin is an extracellular matrix glycoprotein
CC   consisting six disulphide-linked subunits, each having molecular mass of
CC   190-250 kDa.  Tenascin may be important for smooth muscle cell
CC   proliferation as the protein has growth stimulatory activity.  The
CC   polynucleotides can be used to inhibit transcription of the gene or
CC   translation of the mRNA encoding tenascin. The method is applicable to a
CC   number of diseases where the proliferation of smooth muscle is involved
CC   e.g. vascular stenosis, post-angioplasty restenosis and other
CC   non-angioplasty procedures such as cardiac hypertrophy, vascular surgery
CC   and organ transplant.
XX
SQ   Sequence 36 BP; 5 A; 12 C; 8 G; 5 T; 6 other;


  Query Match             100.0%;  Score 17;  DB 15;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 18;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ggccccccatggtggagg 17
           |||||||||||||||||
Db      18 GGCCCCCATGGTGGAGG 2


RESULT   6
AAQ76386
ID   AAQ76386 standard; DNA; 36 BP.
XX
AC   AAQ76386;
XX
DT   01-JUN-1995  (first entry)
XX
DE   Tenascin gene consensus DNA sequence antisense strand.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..36
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                          may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 1; Page 38; 64pp; English.
XX
CC   A series of antisense polynucleotides, either DNA (AAQ76388 and
CC   AAQ77619-32) or RNA (AAQ76390 and AAQ77647-60) directed against the sense
CC   strand of the gene encoding tenascin.  The polynucleotides are based on
CC   the complementary sequence (AAQ76386) of the consensus mRNA initiation
CC   site sequence (AAQ77661) for the tenascin gene.  Tenascin is an
CC   extracellular matrix glycoprotein consisting six disulphide-linked
CC   subunits, each having molecular mass of 190-250 kDa.  Tenascin may be
CC   important for smooth muscle cell proliferation as the protein has growth
CC   stimulatory activity.  The polynucleotides can be used to inhibit
CC   transcription of the gene or translation of the mRNA encoding tenascin.
CC   The method is applicable to a number of diseases where the proliferation
CC   of smooth muscle is involved e.g. vascular stenosis, post-angioplasty
CC   restenosis and other non-angioplasty procedures such as cardiac
CC   hypertrophy, vascular surgery and organ transplant.
XX
SQ   Sequence 36 BP; 5 A; 8 C; 12 G; 5 T; 6 other;


  Query Match             100.0%;  Score 17;  DB 15;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 18;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ggccccccatggtggagg 17
           |||||||||||||||||
Db      19 ggccccccatggtggagg 35


RESULT   7
AAQ77661/c
ID   AAQ77661 standard; RNA; 36 BP.
XX
AC   AAQ77661;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Tenascin gene mRNA initiation site consensus sequence.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Disclosure; Page 7; 64pp; English.
XX
CC   The  consensus sequence surrounding the initiation site of the mRNA for
CC   the tenascin gene.  The sequence was used to generate the corresponding
CC   DNA sequence (AAQ77662).  The sequences were the basis for generating a
CC   series of polynucleotides (AAQ76388-400 and AAQ77614-60) which were
CC   targeted against either the mRNA or the strand coding for the mRNA of the
CC   tenascin gene.  The polynucleotides can be used to inhibit transcription
CC   of the gene or translation of the mRNA encoding tenascin. Tenascin is an
CC   extracellular matrix glycoprotein consisting six disulphide-linked
```

CC subunits, each having molecular mass of 190-250 kDa. Tenascin may be
CC important for smooth muscle cell proliferation as the protein has growth
CC stimulatory activity. The method is applicable to a number of diseases
CC where the proliferation of smooth muscle is involved e.g. vascular
CC stenosis, post-angioplasty restenosis and other non-angioplasty
CC procedures such as cardiac hypertrophy, vascular surgery and organ
CC transplant.
XX
SQ Sequence 36 BP; 5 A; 12 C; 8 G; 5 U; 6 other;

Query Match 100.0%; Score 17; DB 15; Length 36;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ggcccccatggtggagg 17
||||||||||||||||||
Db 18 GGCCCCCATGGTGGAGG 2

RESULT 8
AAQ77662
ID AAQ77662 standard; DNA; 36 BP.
XX
AC AAQ77662;
XX
DT 02-JUN-1995 (first entry)
XX
DE Tenascin gene mRNA initiation site complementary DNA sequence.
XX
KW Antisense; polynucleotide; sense strand; tenascin; complementary;
KW consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW proliferation; growth stimulatory; transcription; vascular stenosis;
KW post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW organ transplant; ds.
XX
OS Synthetic.
XX
PN WO9421664-A.
XX
PD 29-SEP-1994.
XX
PF 24-MAR-1994; 94WO-US03206.
XX
PR 25-MAR-1993; 93US-0037025.
XX
PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI Denner LA, Dixon RAF, Rege AA, Stacy DL;
XX
DR WPI; 1994-316926/39.
XX
PT Synthetic anti-sense polynucleotide - hybridises to tenascin
PT gene, useful for inhibiting vascular smooth muscle cell
PT proliferation.
XX
PS Disclosure; Page 54; 64pp; English.
XX
CC The DNA sequence corresponding to the consensus sequence (AAQ77661)
CC surrounding the initiation site of the mRNA for the tenascin gene. The
CC sequences were the basis for generating a series of polynucleotides
CC (AAQ76386-400 and AAQ77614-60) which were targeted against either the
CC mRNA or the strand coding for the mRNA of the tenascin gene. The
CC polynucleotides can be used to inhibit transcription of the gene or
CC translation of the mRNA encoding tenascin. Tenascin is an extracellular
CC matrix glycoprotein consisting six disulphide-linked subunits, each
CC having molecular mass of 190-250 kDa. Tenascin may be important for
CC smooth muscle cell proliferation as the protein has growth stimulatory
CC activity. The method is applicable to a number of diseases where the
CC proliferation of smooth muscle is involved e.g. vascular stenosis,
CC post-angioplasty restenosis and other non-angioplasty procedures such as
CC cardiac hypertrophy, vascular surgery and organ transplant.
XX
SQ Sequence 36 BP; 5 A; 8 C; 12 G; 5 T; 6 other;

Query Match 100.0%; Score 17; DB 15; Length 36;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ggcccccatggtggagg 17
||||||||||||||||||
Db 19 ggcccccatggtggagg 35

RESULT 9
AAA30431/c
ID AAA30431 standard; cDNA; 33 BP.
XX
AC AAA30431;
XX
DT 11-SEP-2000 (first entry)
XX
DE Human ACAM#6 cDNA 5' PCR primer ACAM-009.
XX
KW Human; cellular adhesion molecule; ACAM; nootropic; antiepileptic;
KW neuroleptic; renal-active; antidiabetic; neuroactive; neuroprotectant;
KW dementia; epilepsy; schizophrenia; peripheral nerve injury;
KW diabetic neuropathy; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200032633-A1.
XX
PD 08-JUN-2000.
XX
PF 02-DEC-1999; 99WO-US28878.
XX
PR 02-DEC-1998; 98US-0203462.
XX
PA (ICOS-) ICOS CORP.
XX
PI Hoekstra DM, Loughney K, Stauton DE, Vazeux R;
XX
DR WPI; 2000-422952/36.
XX
PT Nucleic acids encoding ACAM, a human cellular adhesion molecule, useful
PT for diagnosing, preventing and treating diseases associated with ACAM
PT expression and activity, e.g. epilepsy and schizophrenia -
XX
PS Example 5; Page 97; 187pp; English.
XX
CC The present sequence is a PCR primer used to generate the ACAM#6
CC coding region in an expression construct designed to produce soluble
CC ACAM#6. The primer contains a HindIII site to facilitate ligation of the
CC PCR product into the expression vector. ACAM#6 is a human foetal brain
CC cDNA clone containing the full-length sequence of a novel adhesion
CC molecule designated ACAM. ACAM nucleic acids and polypeptides may be used
CC in the prevention, treatment and diagnosis of diseases associated with
CC inappropriate ACAM expression and activity such as dementia, epilepsy,
CC schizophrenia, peripheral nerve injuries and diabetic neuropathies. They
CC may be used to rectify mutations or deletions in a patient's genome that
CC affect the activity of ACAM or to supplement insufficient ACAM production
CC in a patient. The nucleotide sequence may be integrated into an
CC expression vector and inserted into a host cell for protein expression in
CC vitro or in vivo. Conversely, antisense nucleic acid molecules may be
CC administered to down-regulate ACAM expression. The nucleotide sequence
CC may also be used as a DNA probe in diagnostic assays (e.g. PCR) to detect
CC and quantitate the presence of similar nucleic acid sequences in samples,
CC and hence determine which patients may be in need of restorative therapy.
CC ACAM polypeptides may be used as antigens in the production of antibodies
CC against ACAM and in assays to identify modulators (agonists and
CC antagonists) of ACAM expression and activity.
XX
SQ Sequence 33 BP; 6 A; 16 C; 8 G; 3 T; 0 other;

```
  Query Match             90.6%;  Score 15.4;  DB 21;  Length 33;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 ggccccccatggtggagg 17
           ||||||||||||||| ||
Db      27 GGCCCCCATGGTGGCGG 11


RESULT  10
AAA30437/c
ID   AAA30437 standard; cDNA; 33 BP.
XX
AC   AAA30437;
XX
DT   11-SEP-2000  (first entry)
XX
DE   Human ACAM#4 cDNA 5' PCR primer ACAM-021.
XX
KW   Human; cellular adhesion molecule; ACAM; nootropic; antiepileptic;
KW   neuroleptic; renal-active; antidiabetic; neuroactive; neuroprotectant;
KW   dementia; epilepsy; schizophrenia; peripheral nerve injury;
KW   diabetic neuropathy; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200032633-A1.
XX
PD   08-JUN-2000.
XX
PF   02-DEC-1999;   99WO-US28878.
XX
PR   02-DEC-1998;   98US-0203462.
XX
PA   (ICOS-) ICOS CORP.
XX
PI   Hoekstra DM,  Loughney K,  Stauton DE,  Vazeux R;
XX
DR   WPI; 2000-422952/36.
XX
PT   Nucleic acids encoding ACAM, a human cellular adhesion molecule, useful
PT   for diagnosing, preventing and treating diseases associated with ACAM
PT   expression and activity, e.g. epilepsy and schizophrenia -
XX
PS   Example 5; Page 98; 187pp; English.
XX
CC   The present sequence is a PCR primer used to generate the ACAM#4
CC   coding region in an expression construct designed to produce soluble
CC   ACAM#4. The primer contains a HindIII site to facilitate ligation of the
CC   PCR product into the expression vector. ACAM#4 is a human foetal brain
CC   cDNA clone containing the full-length sequence of a novel adhesion
CC   molecule designated ACAM. ACAM nucleic acids and polypeptides may be used
CC   in the prevention, treatment and diagnosis of diseases associated with
CC   inappropriate ACAM expression and activity such as dementia, epilepsy,
CC   schizophrenia, peripheral nerve injuries and diabetic neuropathies. They
CC   may be used to rectify mutations or deletions in a patient's genome that
CC   affect the activity of ACAM or to supplement insufficient ACAM production
CC   in a patient. The nucleotide sequence may be integrated into an
CC   expression vector and inserted into a host cell for protein expression in
CC   vitro or in vivo. Conversely, antisense nucleic acid molecules may be
CC   administered to down-regulate ACAM expression. The nucleotide sequence
CC   may also be used as a DNA probe in diagnostic assays (e.g. PCR) to detect
CC   and quantitate the presence of similar nucleic acid sequences in samples,
CC   and hence determine which patients may be in need of restorative therapy.
CC   ACAM polypeptides may be used as antigens in the production of antibodies
CC   against ACAM and in assays to identify modulators (agonists and
CC   antagonists) of ACAM expression and activity.
XX
SQ   Sequence 33 BP; 5 A; 16 C; 9 G; 3 T; 0 other;

  Query Match             90.6%;  Score 15.4;  DB 21;  Length 33;
  Best Local Similarity   94.1%;  Pred. No. 1.1e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 ggccccccatggtggagg 17
           ||||||||||||||| ||
Db      27 GGCCCCCATGGTGGCGG 11


RESULT  11
AAQ77617
ID   AAQ77617 standard; DNA; 24 BP.
XX
AC   AAQ77617;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Polynucleotide to tenascin gene consensus mRNA initiation site -6-+18.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..24
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                           may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 5; Page 43; 64pp; English.
XX
CC   A series of polynucleotides, either DNA (AAQ76388 and AAQ76392-400 and
CC   AAQ77614-18) or RNA (AAQ76390 and AAQ77633-46), directed against the
CC   consensus mRNA initiation site sequence (AAQ77661) for the tenascin gene.
CC    The polynucleotides are based on the degenerate sequence (AAQ76386) of
CC   the tenascin gene.  Tenascin is an extracellular matrix glycoprotein
CC   consisting six disulphide-linked subunits, each having molecular mass of
CC   190-250 kDa.  Tenascin may be important for smooth muscle cell
CC   proliferation as the protein has growth stimulatory activity.  The
CC   polynucleotides can be used to inhibit transcription of the gene or
CC   translation of the mRNA encoding tenascin. The method is applicable to a
CC   number of diseases where the proliferation of smooth muscle is involved
CC   e.g. vascular stenosis, post-angioplasty restenosis and other
CC   non-angioplasty procedures such as cardiac hypertrophy, vascular surgery
CC   and organ transplant.
XX
SQ   Sequence 24 BP; 4 A; 7 C; 8 G; 5 T; 0 other;

  Query Match             88.2%;  Score 15;  DB 15;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy      1 ggccccccatggtgga 15
          ||||||||||||||||
Db     10 ggccccccatggtgga 24
```

```
RESULT  12
AAQ77659/c
ID   AAQ77659 standard; RNA; 24 BP.
XX
AC   AAQ77659;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Antisense ribonucleotide binds to tenascin gene consensus at -6-+18.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..24
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                          may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 10; Page 53; 64pp; English.
XX
CC   A series of antisense polynucleotides, either DNA (AAQ76388 and
CC   AAQ77619-32) or RNA (AAQ76390 and AAQ77647-60) directed against the sense
CC   strand of the gene encoding tenascin.  The polynucleotides are based on
CC   the complementary sequence (AAQ76386) of the consensus mRNA initiation
CC   site sequence (AAQ77661) for the tenascin gene.  Tenascin is an
CC   extracellular matrix glycoprotein consisting six disulphide-linked
CC   subunits, each having molecular mass of 190-250 kDa.  Tenascin may be
CC   important for smooth muscle cell proliferation as the protein has growth
CC   stimulatory activity.  The polynucleotides can be used to inhibit
CC   transcription of the gene or translation of the mRNA encoding tenascin.
CC   The method is applicable to a number of diseases where the proliferation
CC   of smooth muscle is involved e.g. vascular stenosis, post-angioplasty
CC   restenosis and other non-angioplasty procedures such as cardiac
CC   hypertrophy, vascular surgery and organ transplant.
XX
SQ   Sequence 24 BP; 5 A; 8 C; 7 G; 4 U; 0 other;
```

```
  Query Match             88.2%;  Score 15;  DB 15;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggccccccatggtgga 15
```

```
          ||||||||||||||||
Db     15 GGCCCCCATGGTGGA 1
```

```
RESULT  13
AAQ77631/c
ID   AAQ77631 standard; DNA; 24 BP.
XX
AC   AAQ77631;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Antisense polynucleotide binds to tenascin gene consensus at -6-+18.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..24
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                          may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 10; Page 46; 64pp; English.
XX
CC   A series of antisense polynucleotides, either DNA (AAQ76388 and
CC   AAQ77619-32) or RNA (AAQ76390 and AAQ77647-60) directed against the sense
CC   strand of the gene encoding tenascin.  The polynucleotides are based on
CC   the complementary sequence (AAQ76386) of the consensus mRNA initiation
CC   site sequence (AAQ77661) for the tenascin gene.  Tenascin is an
CC   extracellular matrix glycoprotein consisting six disulphide-linked
CC   subunits, each having molecular mass of 190-250 kDa.  Tenascin may be
CC   important for smooth muscle cell proliferation as the protein has growth
CC   stimulatory activity.  The polynucleotides can be used to inhibit
CC   transcription of the gene or translation of the mRNA encoding tenascin.
CC   The method is applicable to a number of diseases where the proliferation
CC   of smooth muscle is involved e.g. vascular stenosis, post-angioplasty
CC   restenosis and other non-angioplasty procedures such as cardiac
CC   hypertrophy, vascular surgery and organ transplant.
XX
SQ   Sequence 24 BP; 5 A; 8 C; 7 G; 4 T; 0 other;
```

```
  Query Match             88.2%;  Score 15;  DB 15;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggccccccatggtgga 15
          ||||||||||||||||
Db     15 GGCCCCCATGGTGGA 1
```

```
RESULT  14
AAQ77645
ID   AAQ77645 standard; RNA; 24 BP.
XX
AC   AAQ77645;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Ribonucleotide to tenascin gene consensus mRNA initiation site -6-+18.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..24
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                          may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 5; Page 50; 64pp; English.
XX
CC   A series of polynucleotides, either DNA (AAQ76388 and AAQ76392-400 and
CC   AAQ77614-18) or RNA (AAQ76390 and AAQ77633-46), directed against the
CC   consensus mRNA initiation site sequence (AAQ77661) for the tenascin gene.
CC    The polynucleotides are based on the degenerate sequence (AAQ76386) of
CC   the tenascin gene.  Tenascin is an extracellular matrix glycoprotein
CC   consisting six disulphide-linked subunits, each having molecular mass of
CC   190-250 kDa.  Tenascin may be important for smooth muscle cell
CC   proliferation as the protein has growth stimulatory activity.  The
CC   polynucleotides can be used to inhibit transcription of the gene or
CC   translation of the mRNA encoding tenascin. The method is applicable to a
CC   number of diseases where the proliferation of smooth muscle is involved
CC   e.g. vascular stenosis, post-angioplasty restenosis and other
CC   non-angioplasty procedures such as cardiac hypertrophy, vascular surgery
CC   and organ transplant.
XX
SQ   Sequence 24 BP; 4 A; 7 C; 8 G; 5 U; 0 other;

  Query Match             88.2%;  Score 15;  DB 15;  Length 24;
  Best Local Similarity   86.7%;  Pred. No. 1.7e+02;
  Matches   13;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ggcccccatggtgga 15
           ||||||||:||:|||
Db      10 ggcccccauggugga-24
```

```
RESULT  15
AAV68229
ID   AAV68229 standard; DNA; 34 BP.
XX
AC   AAV68229;
XX
DT   29-JAN-1999  (first entry)
XX
DE   Human cytostatin II primer 4.
XX
KW   ss; human; PCR; primer; amplification; cytostatin; cell growth;
KW   tumour; nervous system; viral infection; microbial infection.
XX
OS   Homo sapiens.
XX
PN   WO9844109-A1.
XX
PD   08-OCT-1998.
XX
PF   25-MAR-1998;   98WO-US05839.
XX
PR   27-MAR-1997;   97US-0041645.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (LONG-) LONG ISLAND JEWISH MEDICAL CENT.
XX
PI   Gentz RL,  Nardelli B,  Ni J,  Shi YE,  Yu G;
XX
DR   WPI; 1998-557110/47.
XX
PT   New isolated human cytostatin II - used to develop products for the
PT   treatment of e.g. cancers or viral or microbial infections or for
PT   protecting nervous system cells from toxic agents.
XX
PS   Example 3; Page 49; 73pp; English.
XX
CC   The primers AAV68226-V68231 were used in the expression of Human
CC   cytostatin, which inhibits cell growth and modulates differentiation.
CC   The cytostatin II polypeptides can be used for inhibiting tumour growth
CC   in a subject, for stimulating growth of or protecting nervous system
CC   cells from toxic agents or for protecting against or treating viral or
CC   microbial infections in mammals.  The products can also be used e.g. to
CC   modulate angiogenesis, to modulate breast development and milk
CC   production.  They can also be used in cerebella granular cells and photo
CC   receptor cells to provide protection from lipid peroxidation associated
CC   with the oxidative stress induced during early stages of ischemia,
CC   apoptosis, and excitatory amino acid induced cell death.  The retinoid
CC   binding potential of cytostatin II may be used on photo receptor cells
CC   in vivo or in vitro.  The activity of haematopoiesis indicates a
CC   possible immunosuppressive activity or a lineage specific stimulation of
CC   haematopoiesis which could be used for treating conditions requiring
CC   immunosuppression.  Antagonists to cytostatin II may be used in vivo to
CC   induce deficiencies or enhancement in the immune or in the
CC   haematopoietic systems.  They may be used e.g. to treat cardiac myocyte
CC   hypertrophy or leukemia.
XX
SQ   Sequence 34 BP; 4 A; 10 C; 12 G; 8 T; 0 other;

  Query Match             84.7%;  Score 14.4;  DB 19;  Length 34;
  Best Local Similarity   93.8%;  Pred. No. 3.4e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 gccccccatggtggagg 17
             ||| ||||||||||||
Db      11 gccaccatggtggagg 26


Search completed: December 21, 2001, 19:24:32
Job time: 11118 sec
```

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: December 21, 2001, 19:24:32 ; Search time 796.8 Seconds
(without alignments)
15.063 Million cell updates/sec

Title: US-09-554-267-5
Perfect score: 14
Sequence: 1 ccccatggtggagg 14

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 989696

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_1101:*
1: /SIDS2/gcgdata/geneseq/geneseqn/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		14	100.0	18	15	AAQ77634	Ribonucleotide to
c 2		14	100.0	18	15	AAQ77620	Antisense polynucl
c 3		14	100.0	18	15	AAQ77648	Antisense ribonucl
4		14	100.0	18	15	AAQ76393	Polynucleotide to
c 5		14	100.0	36	15	AAQ76387	Tenascin gene cons
6		14	100.0	36	15	AAQ76386	Tenascin gene cons
c 7		14	100.0	36	15	AAQ77661	Tenascin gene mRNA
8		14	100.0	36	15	AAQ77662	Tenascin gene mRNA
c 9		12.4	88.6	19	18	AAV01365	Interleukin 4 rece
c 10		12.4	88.6	30	19	AAV24270	Chimeric antibody
c 11		12.4	88.6	30	20	AAX00114	Human antibody PCR
c 12		12.4	88.6	30	21	AAZ58895	PCR primer MBC1HVS
c 13		12.4	88.6	30	22	AAH74267	Nucleotide sequenc
c 14		12.4	88.6	30	22	AAH76626	Humanised anti-PTH
c 15		12.4	88.6	30	22	AAF69111	Human H chain V re
c 16		12.4	88.6	30	22	AAF69167	Human H chain V re
c 17		12.4	88.6	30	22	AAF69223	Human H chain V re
c 18		12.4	88.6	31	21	AAZ58151	Human FAST-1 gene
c 19		12.4	88.6	33	21	AAA30431	Human ACAM#6 cDNA
c 20		12.4	88.6	33	21	AAA30437	Human ACAM#4 cDNA
21		12.4	88.6	34	19	AAV68229	Human cytostatin I
c 22		12.4	88.6	36	19	AAV24252	Chimeric antibody
c 23		12.4	88.6	36	20	AAX00096	Mouse humanised an
c 24		12.4	88.6	36	21	AAA74814	Human erythropoiet
c 25		12.4	88.6	36	21	AAZ58877	PCR primer MBC1HVS
c 26		12.4	88.6	36	22	AAH74251	Nucleotide sequenc
c 27		12.4	88.6	36	22	AAH76608	Human Ig VH PCR pr
c 28		12.4	88.6	36	22	AAF69093	Chimeric antibody
c 29		12.4	88.6	36	22	AAF69149	Chimeric antibody
c 30		12.4	88.6	36	22	AAF69205	Chimeric antibody
31		12.4	88.6	37	15	AAQ69217	PCR primer C3633CC
c 32		12.4	88.6	41	18	AAT97210	Kappa chain variab
c 33		12.4	88.6	41	18	AAT97199	Heavy chain primer
c 34		12.4	88.6	43	17	AAT42077	Human erythropoiet
c 35		12.4	88.6	43	21	AAC60363	Primer EPO-START.
c 36		12.4	88.6	43	22	AAF80219	PCR primer used to
37		12.4	88.6	45	20	AAZ22742	Oligo 2 for immuni
38		12.4	88.6	45	20	AAV64819	Zona pellucida ZP
39		12.4	88.6	45	21	AAZ95679	Recombinant ZPC ve
40		12.4	88.6	45	21	AAZ46287	Expression vector
41		12.4	88.6	45	21	AAZ33276	Recombinant ZPC ve
42		12.4	88.6	45	21	AAZ37826	Oligonucleotide #2
c 43		12	85.7	18	15	AAQ55636	Juniperus Cry j I
44		12	85.7	22	14	AAQ45460	Metastasis inhibit
45		12	85.7	24	15	AAQ77617	Polynucleotide to

ALIGNMENTS

RESULT 1
AAQ77634
ID AAQ77634 standard; RNA; 18 BP.
XX
AC AAQ77634;
XX
DT 02-JUN-1995 (first entry)
XX
DE Ribonucleotide to tenascin gene consensus mRNA initiation site -9-+9.
XX
KW Antisense; polynucleotide; sense strand; tenascin; complementary;
KW consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW proliferation; growth stimulatory; transcription; vascular stenosis;
KW post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW organ transplant; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_difference 1..18
FT /*tag= a
FT /note= "phosphodiester bonds between nucleotides
FT may be replaced by phosphorothioate bonds"
XX
PN WO9421664-A.
XX
PD 29-SEP-1994.
XX
PF 24-MAR-1994; 94WO-US03206.
XX
PR 25-MAR-1993; 93US-0037025.
XX
PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX

```
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 5; Page 47; 64pp; English.
XX
CC   A series of polynucleotides, either DNA (AAQ76388 and AAQ76392-400 and
CC   AAQ77614-18) or RNA (AAQ76390 and AAQ77633-46), directed against the
CC   consensus mRNA initiation site sequence (AAQ77661) for the tenascin gene.
CC    The polynucleotides are based on the degenerate sequence (AAQ76386) of
CC   the tenascin gene.  Tenascin is an extracellular matrix glycoprotein
CC   consisting six disulphide-linked subunits, each having molecular mass of
CC   190-250 kDa.  Tenascin may be important for smooth muscle cell
CC   proliferation as the protein has growth stimulatory activity.  The
CC   polynucleotides can be used to inhibit transcription of the gene or
CC   translation of the mRNA encoding tenascin. The method is applicable to a
CC   number of diseases where the proliferation of smooth muscle is involved
CC   e.g. vascular stenosis, post-angioplasty restenosis and other
CC   non-angioplasty procedures such as cardiac hypertrophy, vascular surgery
CC   and organ transplant.
XX
SQ   Sequence 18 BP; 2 A; 5 C; 8 G; 3 U; 0 other;


  Query Match             100.0%;  Score 14;  DB 15;  Length 18;
  Best Local Similarity   85.7%;  Pred. No. 1.5e+02;
  Matches   12;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ccccatggtggagg 14
          |||||:||:|||||
Db      4 ccccaugguggagg 17


RESULT   2
AAQ77620/c
ID   AAQ77620 standard; DNA; 18 BP.
XX
AC   AAQ77620;
XX
DT   01-JUN-1995  (first entry)
XX
DE   Antisense polynucleotide binds to tenascin gene consensus at -9-+9.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..18
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                          may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 10; Page 44; 64pp; English.
XX
CC   A series of antisense polynucleotides, either DNA (AAQ76388 and
CC   AAQ77619-32) or RNA (AAQ76390 and AAQ77647-60) directed against the sense
CC   strand of the gene encoding tenascin.  The polynucleotides are based on
CC   the complementary sequence (AAQ76386) of the consensus mRNA initiation
CC   site sequence (AAQ77661) for the tenascin gene.  Tenascin is an
CC   extracellular matrix glycoprotein consisting six disulphide-linked
CC   subunits, each having molecular mass of 190-250 kDa.  Tenascin may be
CC   important for smooth muscle cell proliferation as the protein has growth
CC   stimulatory activity.  The polynucleotides can be used to inhibit
CC   transcription of the gene or translation of the mRNA encoding tenascin.
CC   The method is applicable to a number of diseases where the proliferation
CC   of smooth muscle is involved e.g. vascular stenosis, post-angioplasty
CC   restenosis and other non-angioplasty procedures such as cardiac
CC   hypertrophy, vascular surgery and organ transplant.
XX
SQ   Sequence 18 BP; 3 A; 8 C; 5 G; 2 T; 0 other;


  Query Match             100.0%;  Score 14;  DB 15;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ccccatggtggagg 14
          ||||||||||||||
Db     15 CCCCATGGTGGAGG 2


RESULT   3
AAQ77648/c
ID   AAQ77648 standard; RNA; 18 BP.
XX
AC   AAQ77648;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Antisense ribonucleotide binds to tenascin gene consensus at -9-+9.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..18
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                          may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
```

```
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 10; Page 51; 64pp; English.
XX
CC   A series of antisense polynucleotides, either DNA (AAQ76388 and
CC   AAQ77619-32) or RNA (AAQ76390 and AAQ77647-60) directed against the sense
CC   strand of the gene encoding tenascin.  The polynucleotides are based on
CC   the complementary sequence (AAQ76386) of the consensus mRNA initiation
CC   site sequence (AAQ77661) for the tenascin gene.  Tenascin is an
CC   extracellular matrix glycoprotein consisting six disulphide-linked
CC   subunits, each having molecular mass of 190-250 kDa.  Tenascin may be
CC   important for smooth muscle cell proliferation as the protein has growth
CC   stimulatory activity.  The polynucleotides can be used to inhibit
CC   transcription of the gene or translation of the mRNA encoding tenascin.
CC   The method is applicable to a number of diseases where the proliferation
CC   of smooth muscle is involved e.g. vascular stenosis, post-angioplasty
CC   restenosis and other non-angioplasty procedures such as cardiac
CC   hypertrophy, vascular surgery and organ transplant.
XX
SQ   Sequence 18 BP; 3 A; 8 C; 5 G; 2 U; 0 other;


  Query Match             100.0%;  Score 14;  DB 15;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ccccatggtggagg 14
          ||||||||||||||
Db     15 CCCCATGGTGGAGG 2


RESULT   4
AAQ76393
ID   AAQ76393 standard; DNA; 18 BP.
XX
AC   AAQ76393;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Polynucleotide to tenascin gene consensus mRNA initiation site -9-+9.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..18
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                           may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 5; Page 40; 64pp; English.
XX
CC   A series of polynucleotides, either DNA (AAQ76388 and AAQ76392-400 and
CC   AAQ77614-18) or RNA (AAQ76390 and AAQ77633-46), directed against the
CC   consensus mRNA initiation site sequence (AAQ77661) for the tenascin gene.
CC    The polynucleotides are based on the degenerate sequence (AAQ76386) of
CC   the tenascin gene.  Tenascin is an extracellular matrix glycoprotein
CC   consisting six disulphide-linked subunits, each having molecular mass of
CC   190-250 kDa.  Tenascin may be important for smooth muscle cell
CC   proliferation as the protein has growth stimulatory activity.  The
CC   polynucleotides can be used to inhibit transcription of the gene or
CC   translation of the mRNA encoding tenascin. The method is applicable to a
CC   number of diseases where the proliferation of smooth muscle is involved
CC   e.g. vascular stenosis, post-angioplasty restenosis and other
CC   non-angioplasty procedures such as cardiac hypertrophy, vascular surgery
CC   and organ transplant.
XX
SQ   Sequence 18 BP; 2 A; 5 C; 8 G; 3 T; 0 other;


  Query Match             100.0%;  Score 14;  DB 15;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ccccatggtggagg 14
          ||||||||||||||
Db      4 ccccatggtggagg 17


RESULT   5
AAQ76387/c
ID   AAQ76387 standard; DNA; 36 BP.
XX
AC   AAQ76387;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Tenascin gene consensus DNA sequence sense strand.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..36
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                           may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
```

PS Claim 6; Page 39; 64pp; English.
XX
CC A series of polynucleotides, either DNA (AAQ76389 and AAQ76392-400 and
CC AAQ77614-18) or RNA (AAQ76391 and AAQ77633-46), directed against the
CC consensus mRNA initiation site sequence (AAQ77661) for the tenascin gene.
CC The polynucleotides are based on the sense strand sequence (AAQ76387) of
CC the tenascin gene. Tenascin is an extracellular matrix glycoprotein
CC consisting six disulphide-linked subunits, each having molecular mass of
CC 190-250 kDa. Tenascin may be important for smooth muscle cell
CC proliferation as the protein has growth stimulatory activity. The
CC polynucleotides can be used to inhibit transcription of the gene or
CC translation of the mRNA encoding tenascin. The method is applicable to a
CC number of diseases where the proliferation of smooth muscle is involved
CC e.g. vascular stenosis, post-angioplasty restenosis and other
CC non-angioplasty procedures such as cardiac hypertrophy, vascular surgery
CC and organ transplant.
XX
SQ Sequence 36 BP; 5 A; 12 C; 8 G; 5 T; 6 other;

Query Match 100.0%; Score 14; DB 15; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ccccatggtggagg 14
||||||||||||||
Db 15 CCCCATGGTGGAGG 2

RESULT 6
AAQ76386
ID AAQ76386 standard; DNA; 36 BP.
XX
AC AAQ76386;
XX
DT 01-JUN-1995 (first entry)
XX
DE Tenascin gene consensus DNA sequence antisense strand.
XX
KW Antisense; polynucleotide; sense strand; tenascin; complementary;
KW consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW proliferation; growth stimulatory; transcription; vascular stenosis;
KW post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW organ transplant; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_difference 1..36
FT /*tag= a
FT /note= "phosphodiester bonds between nucleotides
FT may be replaced by phosphorothioate bonds"
XX
PN WO9421664-A.
XX
PD 29-SEP-1994.
XX
PF 24-MAR-1994; 94WO-US03206.
XX
PR 25-MAR-1993; 93US-0037025.
XX
PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI Denner LA, Dixon RAF, Rege AA, Stacy DL;
XX
DR WPI; 1994-316926/39.
XX
PT Synthetic anti-sense polynucleotide - hybridises to tenascin
PT gene, useful for inhibiting vascular smooth muscle cell
PT proliferation.
XX
PS Claim 1; Page 38; 64pp; English.
XX
CC A series of antisense polynucleotides, either DNA (AAQ76388 and
CC AAQ77619-32) or RNA (AAQ76390 and AAQ77647-60) directed against the sense
CC strand of the gene encoding tenascin. The polynucleotides are based on
CC the complementary sequence (AAQ76386) of the consensus mRNA initiation
CC site sequence (AAQ77661) for the tenascin gene. Tenascin is an
CC extracellular matrix glycoprotein consisting six disulphide-linked
CC subunits, each having molecular mass of 190-250 kDa. Tenascin may be
CC important for smooth muscle cell proliferation as the protein has growth
CC stimulatory activity. The polynucleotides can be used to inhibit
CC transcription of the gene or translation of the mRNA encoding tenascin.
CC The method is applicable to a number of diseases where the proliferation
CC of smooth muscle is involved e.g. vascular stenosis, post-angioplasty
CC restenosis and other non-angioplasty procedures such as cardiac
CC hypertrophy, vascular surgery and organ transplant.
XX
SQ Sequence 36 BP; 5 A; 8 C; 12 G; 5 T; 6 other;

Query Match 100.0%; Score 14; DB 15; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ccccatggtggagg 14
||||||||||||||
Db 22 ccccatggtggagg 35

RESULT 7
AAQ77661/c
ID AAQ77661 standard; RNA; 36 BP.
XX
AC AAQ77661;
XX
DT 02-JUN-1995 (first entry)
XX
DE Tenascin gene mRNA initiation site consensus sequence.
XX
KW Antisense; polynucleotide; sense strand; tenascin; complementary;
KW consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW proliferation; growth stimulatory; transcription; vascular stenosis;
KW post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW organ transplant; ds.
XX
OS Synthetic.
XX
PN WO9421664-A.
XX
PD 29-SEP-1994.
XX
PF 24-MAR-1994; 94WO-US03206.
XX
PR 25-MAR-1993; 93US-0037025.
XX
PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI Denner LA, Dixon RAF, Rege AA, Stacy DL;
XX
DR WPI; 1994-316926/39.
XX
PT Synthetic anti-sense polynucleotide - hybridises to tenascin
PT gene, useful for inhibiting vascular smooth muscle cell
PT proliferation.
XX
PS Disclosure; Page 7; 64pp; English.
XX
CC The consensus sequence surrounding the initiation site of the mRNA for
CC the tenascin gene. The sequence was used to generate the corresponding
CC DNA sequence (AAQ77662). The sequences were the basis for generating a
CC series of polynucleotides (AAQ76388-400 and AAQ77614-60) which were
CC targeted against either the mRNA or the strand coding for the mRNA of the
CC tenascin gene. The polynucleotides can be used to inhibit transcription
CC of the gene or translation of the mRNA encoding tenascin. Tenascin is an
CC extracellular matrix glycoprotein consisting six disulphide-linked

```
CC   subunits, each having molecular mass of 190-250 kDa.  Tenascin may be
CC   important for smooth muscle cell proliferation as the protein has growth
CC   stimulatory activity.  The method is applicable to a number of diseases
CC   where the proliferation of smooth muscle is involved e.g. vascular
CC   stenosis, post-angioplasty restenosis and other non-angioplasty
CC   procedures such as cardiac hypertrophy, vascular surgery and organ
CC   transplant.
XX
SQ   Sequence 36 BP; 5 A; 12 C; 8 G; 5 U; 6 other;


  Query Match             100.0%;  Score 14;  DB 15;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ccccatggtggagg 14
          ||||||||||||||
Db     15 CCCCATGGTGGAGG 2


RESULT   8
AAQ77662
ID   AAQ77662 standard; DNA; 36 BP.
XX
AC   AAQ77662;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Tenascin gene mRNA initiation site complementary DNA sequence.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Disclosure; Page 54; 64pp; English.
XX
CC   The DNA sequence corresponding to the consensus sequence (AAQ77661)
CC   surrounding the initiation site of the mRNA for the tenascin gene.  The
CC   sequences were the basis for generating a series of polynucleotides
CC   (AAQ76386-400 and AAQ77614-60) which were targeted against either the
CC   mRNA or the strand coding for the mRNA of the tenascin gene.  The
CC   polynucleotides can be used to inhibit transcription of the gene or
CC   translation of the mRNA encoding tenascin. Tenascin is an extracellular
CC   matrix glycoprotein consisting six disulphide-linked subunits, each
CC   having molecular mass of 190-250 kDa.  Tenascin may be important for
CC   smooth muscle cell proliferation as the protein has growth stimulatory
CC   activity.  The method is applicable to a number of diseases where the
CC   proliferation of smooth muscle is involved e.g. vascular stenosis,
CC   post-angioplasty restenosis and other non-angioplasty procedures such as
CC   cardiac hypertrophy, vascular surgery and organ transplant.
XX
SQ   Sequence 36 BP; 5 A; 8 C; 12 G; 5 T; 6 other;


  Query Match             100.0%;  Score 14;  DB 15;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ccccatggtggagg 14
          ||||||||||||||
Db     22 ccccatggtggagg 35


RESULT   9
AAV01365/c
ID   AAV01365 standard; DNA; 19 BP.
XX
AC   AAV01365;
XX
DT   23-MAR-1998  (first entry)
XX
DE   Interleukin 4 receptor PCR primer for universal mammalian STS's.
XX
KW   PCR primer; polymerase chain reaction; amplification; UM-STS;
KW   universal mammalian sequence tagged site; genomic map; clone; ss.
XX
OS   Synthetic.
XX
PN   WO9731012-A1.
XX
PD   28-AUG-1997.
XX
PF   18-FEB-1997;   97WO-US02403.
XX
PR   22-FEB-1996;   96US-0012061.
XX
PA   (UNMI ) UNIV MICHIGAN.
PA   (UNMS ) UNIV MICHIGAN STATE.
XX
PI   Brewer GJ,  Venta PJ,  Yuzbasiyan-Gurkan V;
XX
DR   WPI; 1997-435083/40.
XX
PT   New oligonucleotide primers amplifying gene regions conserved among
PT   mammals - useful for developing genomic maps, isolating clones and
PT   making cross-species comparisons
XX
PS   Claim 2; Page 13; 26pp; English.
XX
CC   The present sequence represents a specifically claimed oligonucleotide
CC   PCR primer. The oligonucleotide can be used for polymerase chain
CC   reaction (PCR) amplification of DNA, specifically regions of specific
CC   genes that are conserved among mammalian species, i.e. pairs of
CC   oligonucleotides from the present specification represent universal
CC   mammalian sequence-tagged site (UM-STS) primers. The primers are used
CC   to develop genomic maps, to isolate clones from libraries, to make
CC   cross-species comparisons and to develop additional genetic markers.
CC   UM-STS allow genomic comparisons to be made between more species.
XX
SQ   Sequence 19 BP; 3 A; 6 C; 7 G; 3 T; 0 other;


  Query Match             88.6%;  Score 12.4;  DB 18;  Length 19;
  Best Local Similarity   92.9%;  Pred. No. 1.1e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 ccccatggtggagg 14
          ||||||| ||||||
Db     16 CCCCATGCTGGAGG 3


RESULT  10
AAV24270/c
ID   AAV24270 standard; DNA; 30 BP.
```

```
XX
AC   AAV24270;
XX
DT   03-SEP-1998  (first entry)
XX
DE   Chimeric antibody against hPTRP human H chain PCR primer MBC1HVS1.
XX
KW   Chimeric; antibody; human parathormone related peptide; hPTRP; mouse;
KW   L chain; H chain; hypercalcaemia; cancer; malignant lymphoma; CDR;
KW   hypophosphaemia; pathogen; vitamin D resistance; V region; C region;
KW   humanised; PCR primer ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9813388-A1.
XX
PD   02-APR-1998.
XX
PF   24-SEP-1997;   97WO-JP03382.
XX
PR   24-JUL-1997;   97JP-0214168.
PR   26-SEP-1996;   96JP-0255196.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
PI   Sato K,  Wakahara Y,  Yabuta N;
XX
DR   WPI; 1998-230640/20.
XX
PT   New chimeric antibodies against human parathormone related
PT   peptide(s) - useful for, e.g. treatment of hypercalcaemia and other
PT   disorders caused by malignant neoplasm(s)
XX
PS   Example 3; Page 105; 182pp; Japanese.
XX
CC   New antibodies have been developed which are specific for human
CC   parathormone related peptides (hPTRP). The antibodies comprise chimeric
CC   L and/or H chains, where the C region is of human and L region of mouse,
CC   origin. The present sequence represents a PCR primer used in an example
CC   of the present invention. Host cells, transformed with vectors
CC   containing DNA encoding antibodies of the invention, can be used to
CC   produce the antibodies. The antibodies may be used to treat
CC   hypercalcaemia, especially that due to a malignancy, e.g. cancers of
CC   pancreas, lung, throat, larynx, tongue, gum, oesophagus, stomach, liver,
CC   breast, kidney, bladder, womb or prostate or malignant lymphoma. They
CC   may also be used for treatment of hypophosphaemia such as that due to
CC   pathogens or to vitamin D resistance.
XX
SQ   Sequence 30 BP; 4 A; 7 C; 10 G; 9 T; 0 other;


  Query Match             88.6%;  Score 12.4;  DB 19;  Length 30;
  Best Local Similarity   92.9%;  Pred. No. 1.1e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 ccccatggtggagg 14
          ||||||||||||| |
Db     21 CCCCATGGTGGAAG 8


RESULT  11
AAX00114/c
ID   AAX00114 standard; DNA; 30 BP.
XX
AC   AAX00114;
XX
DT   14-APR-1999  (first entry)
XX
DE   Human antibody PCR primer MBC1HVS1.
XX
KW   Human; parathyroid hormone related protein; PTHrP; cachexia; cancer;
KW   inhibitor; humanised; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9851329-A1.
XX
PD   19-NOV-1998.
XX
PF   13-MAY-1998;   98WO-JP02116.
XX
PR   18-JUL-1997;   97JP-0194445.
PR   15-MAY-1997;   97JP-0125505.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
PI   Ishii K,  Sato K,  Tunenari T;
XX
DR   WPI; 1999-070101/06.
XX
PT   Inhibitors of binding of parathyroid hormone related peptide to its
PT   receptor - useful for, e.g. treatment of cachexia arising from
PT   cancer or other diseases
XX
PS   Example 4; Page 66; 125pp; Japanese.
XX
CC   The present invention describes compositions for the treatment of
CC   cachexia containing a substance which inhibits the binding of a
CC   parathyroid hormone related peptide (PTHrP) to its receptor, as an
CC   active component. This substance may be an antagonist to the receptor,
CC   or an antibody (preferably monoclonal) or antibody fragment,
CC   recognising PTHrP. The antibody is preferably humanised or chimeric.
CC   The present invention also describes a humanised antibody prepared
CC   by hybridoma 23-57-137-1 (FERM BP-5631). The composition is used for
CC   the treatment of cachexia arising in connection with diseases such as
CC   cancer, thereby improving the quality of life of the patient. The
CC   present sequence represents a PCR primer used in an example from the
CC   present invention.
XX
SQ   Sequence 30 BP; 4 A; 7 C; 10 G; 9 T; 0 other;


  Query Match             88.6%;  Score 12.4;  DB 20;  Length 30;
  Best Local Similarity   92.9%;  Pred. No. 1.1e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 ccccatggtggagg 14
          ||||||||||||| |
Db     21 CCCCATGGTGGAAG 8


RESULT  12
AAZ58895/c
ID   AAZ58895 standard; DNA; 30 BP.
XX
AC   AAZ58895;
XX
DT   26-APR-2000  (first entry)
XX
DE   PCR primer MBC1HVS1.
XX
KW   Hypercalcemic crisis; parathyroid hormone related peptide; PTHrP;
KW   human; tumour; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200000219-A1.
XX
PD   06-JAN-2000.
XX
PF   25-JUN-1999;   99WO-JP03433.
XX
PR   26-JUN-1998;   98JP-0180143.
XX
```

PA (CHUS) CHUGAI SEIYAKU KK.
XX
PI Sato K, Tsunenari T;
XX
DR WPI; 2000-117115/10.
XX
PT Treatment of hypercalcemic crisis with a substance inhibiting binding
PT of parathyroid hormone related peptide to its receptor -
XX
PS Example 4; Page 80; 120pp; Japanese.
XX
CC The invention relates to a method of treatment of hypercalcemic crisis.
CC A composition for the treatment of hypercalcemic crisis contains as
CC active component a substance which inhibits the binding of parathyroid
CC hormone related peptide (PTHrP) to its receptor. The inhibitor is used
CC for the treatment of hypercalcemic crisis, such as that associated with
CC a malignant tumour.
XX
SQ Sequence 30 BP; 4 A; 7 C; 10 G; 9 T; 0 other;

Query Match 88.6%; Score 12.4; DB 21; Length 30;
Best Local Similarity 92.9%; Pred. No. 1.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ccccatggtggagg 14
||||||||||||| |
Db 21 CCCCATGGTGGAAG 8

RESULT 13
AAH74267/c
ID AAH74267 standard; DNA; 30 BP.
XX
AC AAH74267;
XX
DT 15-OCT-2001 (first entry)
XX
DE Nucleotide sequence of an oligonucleotide.
XX
KW Parathyroid hormone-associated peptide; PTHrP; dental disease; primer;
KW ss.
XX
OS Synthetic.
XX
PN WO200154725-A1.
XX
PD 02-AUG-2001.
XX
PF 14-DEC-2000; 2000WO-JP08875.
XX
PR 25-JAN-2000; 2000JP-0083034.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
XX
PI Kato A, Suzuki M, Sugimoto T;
XX
DR WPI; 2001-465459/50.
XX
PT Parathyroid hormone-associated peptide binding inhibitors useful for
PT treating dental disease -
XX
PS Example 4; Page 92; 140pp; Japanese.
XX
CC The present oligonucleotide was used in the course of the invention.
CC The specification describes a treatment for dental diseases. The
CC treatment comprises a substance that inhibits binding between
CC parathyroid hormone-associated peptide and its receptor.
XX
SQ Sequence 30 BP; 4 A; 7 C; 10 G; 9 T; 0 other;

Query Match 88.6%; Score 12.4; DB 22; Length 30;
Best Local Similarity 92.9%; Pred. No. 1.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ccccatggtggagg 14
||||||||||||| |
Db 21 CCCCATGGTGGAAG 8

RESULT 14
AAH76626/c
ID AAH76626 standard; DNA; 30 BP.
XX
AC AAH76626;
XX
DT 08-OCT-2001 (first entry)
XX
DE Humanised anti-PTHrP Ab VH CDR PCR primer MBC1HVS1, SEQ ID NO:27.
XX
KW Parathyroid hormone-related peptide; PTHrP; antagonist; antibody;
KW calcium regulation disorder; serum calcium concentration;
KW humoral hypercalcaemia of malignancy; cytostatic; analgesic;
KW PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200147554-A1.
XX
PD 05-JUL-2001.
XX
PF 27-DEC-2000; 2000WO-JP09339.
XX
PR 28-DEC-1999; 99JP-0375203.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
XX
PI Yamazaki T, Hayasaka A, Koga A;
XX
DR WPI; 2001-425590/45.
XX
PT Composition for treating diseases of calcium regulation and for use as
PT an analgesic, comprises an antibody recognizing parathyroid hormone
PT related peptide -
XX
PS Examples; Page 87; 128pp; Japanese.
XX
CC The invention relates to a stabilised composition of an antibody which
CC recognises parathyroid hormone-related peptide (PTHrP) - see AAG64793.
CC The composition consists of a solution of the antibody in a buffer of pH
CC 5-8 containing one or more of acetic acid, phosphoric acid, citric acid
CC and their salts. The composition has increased storage stability,
CC especially at elevated temperatures. The composition antagonises the
CC action of PTHrP, and may be used in the treatment of diseases involving
CC disturbances of calcium regulation (high or low serum calcium
CC concentration) such as humoral hypercalcaemia of malignancy and as an
CC analgesic. The present sequence represents a PCR primer used in the
CC exemplifications of the invention in the construction of polynucleotides
CC encoding humanised versions of the anti-human PTHrP murine monoclonal
CC antibody 23-57-137-1.
XX
SQ Sequence 30 BP; 4 A; 7 C; 10 G; 9 T; 0 other;

Query Match 88.6%; Score 12.4; DB 22; Length 30;
Best Local Similarity 92.9%; Pred. No. 1.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ccccatggtggagg 14
||||||||||||| |
Db 21 CCCCATGGTGGAAG 8

RESULT 15
AAF69111/c

ID AAF69111 standard; DNA; 30 BP.
XX
AC AAF69111;
XX
DT 12-APR-2001 (first entry)
XX
DE Human H chain V region PCR primer MBC1HVS1 SEQ ID NO:27.
XX
KW Human; mouse; parathyroid hormone-related peptide; PTHrP; vasopressin;
KW monoclonal antibody; antidiarrheic; antiemetic; antidiabetic;
KW antipyretic; cancer; dehydration; excessive urination; thirst;
KW vomiting; diarrhoea; fever; perspiration; diabetes; PCR primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200102010-A1.
XX
PD 11-JAN-2001.
XX
PF 03-JUL-2000; 2000WO-JP04413.
XX
PR 02-JUL-1999; 99JP-0189322.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
XX
PI Ogata E, Onuma E, Tsunenari T, Saito H, Azuma Y;
XX
DR WPI; 2001-112507/12.
XX
PT Inhibitor of parathyroid hormone related peptide binding to its
PT receptor can ameliorate symptoms caused by a decrease in vasopressin
PT level due to cancer -
XX
PS Example 2; Page 72; 114pp; Japanese.
XX
CC The present invention describes an agent (I) for ameliorating low
CC vasopressin levels, and symptoms caused by this depression, containing
CC as an active component a substance which inhibits the binding of
CC parathyroid hormone related peptide (PTHrP) to its receptor. (I) has
CC antidiarrheic, antiemetic, antidiabetic and antipyretic activities.
CC (I) can be used for the amelioration of symptoms caused by decrease in
CC vasopressin levels, such as that due to cancer are treated using the
CC agent. These symptoms include dehydration, excessive urination, thirst,
CC vomiting, diarrhoea, fever, perspiration and diabetes. AAF69085 to
CC AAF69140 and AAB76879 to AAB76897 represent sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 30 BP; 4 A; 7 C; 10 G; 9 T; 0 other;

Query Match 88.6%; Score 12.4; DB 22; Length 30;
Best Local Similarity 92.9%; Pred. No. 1.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ccccatggtggagg 14
||||||||||||| |
Db 21 CCCCATGGTGGAAG 8

Search completed: December 21, 2001, 19:24:33
Job time: 11119 sec

```
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unidentified"
                     /db_xref="taxon:32644"
     exon            1. .16
BASE COUNT        3 a      4 c      4 g      5 t
ORIGIN


  Query Match             100.0%;  Score 16;  DB 13;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 agttgcctggacattc 16
          ||||||||||||||||
Db      1 AGTTGCCTGGACATTC 16


RESULT   5
AX030510
LOCUS       AX030510        16 bp    DNA             UNA       20-SEP-2000
DEFINITION  Sequence 30 from Patent DE19750702.
ACCESSION   AX030510
VERSION     AX030510.1  GI:10278067
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Peyman,A.D., Uhlmann,E.D. and Weiser,C.D.
  TITLE     Antisense oligonucleotides that bind to sequences encoding human
            tenascin for treating depigmentation, cancer, inflammation and
            cardiovascular disease
  JOURNAL   Patent: DE 19750702-A 27-MAY-1999;
            HOECHST MARION ROUSSEL DE GMBH (DE)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        3 a      4 c      4 g      5 t
ORIGIN


  Query Match             100.0%;  Score 16;  DB 13;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 agttgcctggacattc 16
          ||||||||||||||||
Db      1 AGTTGCCTGGACATTC 16


RESULT   6
AX030529
LOCUS       AX030529        16 bp    DNA             UNA       20-SEP-2000
DEFINITION  Sequence 49 from Patent DE19750702.
ACCESSION   AX030529
VERSION     AX030529.1  GI:10278086
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Peyman,A.D., Uhlmann,E.D. and Weiser,C.D.
  TITLE     Antisense oligonucleotides that bind to sequences encoding human
            tenascin for treating depigmentation, cancer, inflammation and
            cardiovascular disease
  JOURNAL   Patent: DE 19750702-A 27-MAY-1999;
            HOECHST MARION ROUSSEL DE GMBH (DE)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        3 a      4 c      4 g      5 t
ORIGIN


  Query Match             100.0%;  Score 16;  DB 13;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 agttgcctggacattc 16
          ||||||||||||||||
Db      1 AGTTGCCTGGACATTC 16


RESULT   7
C75717/c
LOCUS       C75717          35 bp    DNA             STS       12-FEB-1999
DEFINITION  Homo sapiens STS D21S1255, DH PROBE, FORWARD PRIMER, sequence
            tagged site.
ACCESSION   C75717
VERSION     C75717.1  GI:3176159
KEYWORDS    STS; DH; Digital hybridization.
SOURCE      Homo sapiens DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 35)
  AUTHORS   Asakawa,S. and Shimizu,N.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-SEP-1997) to the DDBJ/EMBL/GenBank databases. Shuichi
            Asakawa, Keio University School of Medicine; Department of
            Molecular Biology; Shinanomachi 35, Shinjuku-ku, Tokyo 160, Japan
            (E-mail:asa@dmb.med.keio.ac.jp, Tel:81-3-3351-2370)
REFERENCE   2  (sites)
  AUTHORS   Asakawa,S. and Shimizu,N.
  TITLE     High-fidelity digital hybridization screening
  JOURNAL   Genomics 49 (2), 209-217 (1998)
  MEDLINE   98260670
FEATURES             Location/Qualifiers
     source          1. .35
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT       15 a      6 c     11 g      3 t
ORIGIN


  Query Match             77.5%;  Score 12.4;  DB 77;  Length 35;
  Best Local Similarity   92.9%;  Pred. No. 5.6e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 ttgcctggacattc 16
          |||||||||||| |
Db     27 TTGCCTGGACATCC 14


RESULT   8
I43351/c
LOCUS       I43351          35 bp    DNA             PAT       07-OCT-1997
DEFINITION  Sequence 5 from patent US 5631150.
ACCESSION   I43351
VERSION     I43351.1  GI:2468595
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 35)
  AUTHORS   Harkki,A.M., Myasnikov,A.N., Apajalahti,J.H.A. and Pastinen,O.A.
  TITLE     Manufacturing of xylitol using recombinant microbial hosts
  JOURNAL   Patent: US 5631150-A 5 20-MAY-1997;
FEATURES             Location/Qualifiers
     source          1. .35
                     /organism="unknown"
BASE COUNT       13 a      8 c      9 g      5 t
ORIGIN
```

```
  Query Match             77.5%;  Score 12.4;  DB 81;  Length 35;
  Best Local Similarity   92.9%;  Pred. No. 5.6e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 gttgcctggacatt 15
          ||||| ||||||||
Db     26 GTTGCTTGGACATT 13


RESULT   9
HSZ74612
LOCUS       HSZ74612       41 bp    DNA             PRI       19-DEC-1996
DEFINITION  H.sapiens jak3 gene (intron XVIII acceptor).
ACCESSION   Z74612
VERSION     Z74612.1  GI:1747401
KEYWORDS    JAK3 gene; splice junction.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 41)
  AUTHORS   Villa,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-JUN-1996) A. Villa, ITBA- CNR, Via Ampere 56, I-20131
            Milan, ITALY
REFERENCE   2  (bases 1 to 41)
  AUTHORS   Villa,A., Sironi,M., Macchi,P. and Mantovani,A.
  TITLE     Monocyte function in a SCID patient with a donor splice site
            mutation in the JAK3
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 41)
  AUTHORS   Villa,A., Sironi,M., Macchi,P., Matteucci,C., Notarangelo,L.D.,
            Vezzoni,P. and Mantovani,A.
  TITLE     Monocyte function in a severe combined immunodeficient patient with
            a donor splice site mutation in the Jak3 gene
  JOURNAL   Blood 88 (3), 817-823 (1996)
  MEDLINE   96309622
FEATURES             Location/Qualifiers
     source          1. .41
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /tissue_type="peripheral blood"
     gene            1. .41
                     /gene="jak3"
     intron          1. .41
                     /partial
                     /gene="jak3"
                     /note="splice junction, acceptor site"
                     /number=18
BASE COUNT        8 a      17 c       9 g       7 t
ORIGIN


  Query Match             77.5%;  Score 12.4;  DB 53;  Length 41;
  Best Local Similarity   92.9%;  Pred. No. 5.6e+03;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 agttgcctggacat 14
            || ||||||||||
Db      9 AGGTGCCTGGACAT 22


RESULT  10
A41487/c
LOCUS       A41487         24 bp    DNA             PAT       05-MAR-1997
DEFINITION  Sequence 2 from Patent WO9428129.
ACCESSION   A41487
VERSION     A41487.1  GI:2297141
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Tarin,D.
  TITLE     TUMOUR METASTASIS GENE
  JOURNAL   Patent: WO 9428129-A 2 08-DEC-1994;
            ISIS INNOVATION (GB)
COMMENT     Other publication AU 6802294 941220.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        7 a      8 c      6 g      3 t
ORIGIN


  Query Match             75.0%;  Score 12;  DB 81;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 gcctggacattc 16
          ||||||||||||
Db     22 GCCTGGACATTC 11


RESULT  11
AR090533/c
LOCUS       AR090533       26 bp    DNA             PAT       07-SEP-2000
DEFINITION  Sequence 653 from patent US 5994076.
ACCESSION   AR090533
VERSION     AR090533.1  GI:10017288
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
  TITLE     Methods of assaying differential expression
  JOURNAL   Patent: US 5994076-A 653 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
BASE COUNT        8 a      8 c      6 g      4 t
ORIGIN


  Query Match             71.2%;  Score 11.4;  DB 81;  Length 26;
  Best Local Similarity   92.3%;  Pred. No. 2.5e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 ttgcctggacatt 15
          | ||||||||||||
Db     15 TGGCCTGGACATT 3


RESULT  12
A14221/c
LOCUS       A14221         30 bp    DNA             PAT       27-MAR-1994
DEFINITION  oligonucleotide 85.
ACCESSION   A14221
VERSION     A14221.1  GI:513743
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Markham,A.F., Smith,J.C. and Anwar,R.
  TITLE     A method for the amplification of nucleotide sequences
  JOURNAL   Patent: EP 0356021-A 102 28-FEB-1990;
            IMPERIAL CHEMICAL INDUSTRIES PLC
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unidentified"
                     /db_xref="taxon:32644"
```

```
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /db_xref="taxon:32644"
     exon            1. .15
BASE COUNT        0 a      4 c      6 g      5 t
ORIGIN


  Query Match             100.0%;  Score 15;  DB 13;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tgtcgcttgtgccgg 15
          |||||||||||||||
Db      1 TGTCGCTTGTGCCGG 15


RESULT   5
AX030511
LOCUS       AX030511       15 bp    DNA             UNA       20-SEP-2000
DEFINITION  Sequence 31 from Patent DE19750702.
ACCESSION   AX030511
VERSION     AX030511.1  GI:10278068
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Peyman,A.D., Uhlmann,E.D. and Weiser,C.D.
  TITLE     Antisense oligonucleotides that bind to sequences encoding human
            tenascin for treating depigmentation, cancer, inflammation and
            cardiovascular disease
  JOURNAL   Patent: DE 19750702-A 27-MAY-1999;
            HOECHST MARION ROUSSEL DE GMBH (DE)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        0 a      4 c      6 g      5 t
ORIGIN


  Query Match             100.0%;  Score 15;  DB 13;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tgtcgcttgtgccgg 15
          |||||||||||||||
Db      1 TGTCGCTTGTGCCGG 15


RESULT   6
AX030530
LOCUS       AX030530       15 bp    DNA             UNA       20-SEP-2000
DEFINITION  Sequence 50 from Patent DE19750702.
ACCESSION   AX030530
VERSION     AX030530.1  GI:10278087
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Peyman,A.D., Uhlmann,E.D. and Weiser,C.D.
  TITLE     Antisense oligonucleotides that bind to sequences encoding human
            tenascin for treating depigmentation, cancer, inflammation and
            cardiovascular disease
  JOURNAL   Patent: DE 19750702-A 27-MAY-1999;
            HOECHST MARION ROUSSEL DE GMBH (DE)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        0 a      4 c      6 g      5 t
ORIGIN


  Query Match             100.0%;  Score 15;  DB 13;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tgtcgcttgtgccgg 15
          |||||||||||||||
Db      1 TGTCGCTTGTGCCGG 15


RESULT   7
AR090333/c
LOCUS       AR090333       25 bp    DNA             PAT       07-SEP-2000
DEFINITION  Sequence 453 from patent US 5994076.
ACCESSION   AR090333
VERSION     AR090333.1  GI:10017088
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
  TITLE     Methods of assaying differential expression
  JOURNAL   Patent: US 5994076-A 453 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
BASE COUNT        6 a      9 c      8 g      2 t
ORIGIN


  Query Match             78.7%;  Score 11.8;  DB 81;  Length 25;
  Best Local Similarity   86.7%;  Pred. No. 8.7e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tgtcgcttgtgccgg 15
          || |||||||| |||
Db     23 TGGCGCTTGTGTCGG 9


RESULT   8
AR020695
LOCUS       AR020695       39 bp    DNA             PAT       05-DEC-1998
DEFINITION  Sequence 105 from patent US 5789184.
ACCESSION   AR020695
VERSION     AR020695.1  GI:3975310
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   Fowlkes,D.M., Broach,J., Manfredi,J., Klein,C., Murphy,A.J.,
            Paul,J. and Trueheart,J.
  TITLE     Yeast cells engineered to produce pheromone system protein
            surrogates, and uses therefor
  JOURNAL   Patent: US 5789184-A 105 04-AUG-1998;
FEATURES             Location/Qualifiers
     source          1. .39
                     /organism="unknown"
BASE COUNT        4 a      11 c     13 g     11 t
ORIGIN


  Query Match             78.7%;  Score 11.8;  DB 81;  Length 39;
  Best Local Similarity   86.7%;  Pred. No. 8e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tgtcgcttgtgccgg 15
          ||||||| || ||||
Db     11 TGTCGCTCGTCCCGG 25
```

```
RESULT   9
AR028729/c
LOCUS       AR028729       20 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 18 from patent US 5858760.
ACCESSION   AR028729
VERSION     AR028729.1  GI:5940702
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dalb.o slashed.ge,H., Kofod,L.Venke, Kauppinen,M.Sakari,
            Andersen,L.Nonboe, Christgau,S. and Heldt-Hansen,H.Peter.
  TITLE     Enzyme with pectin lyase activity
  JOURNAL   Patent: US 5858760-A 18 12-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        5 a      9 c      5 g      1 t
ORIGIN


  Query Match             76.0%;  Score 11.4;  DB 81;  Length 20;
  Best Local Similarity   92.3%;  Pred. No. 1.5e+05;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 gtcgcttgtgccg 14
          | ||||||||||||
Db     16 GGCGCTTGTGCCG 4


RESULT  10
A83807/c
LOCUS       A83807         23 bp    DNA             PAT       21-JAN-2000
DEFINITION  Sequence 13 from Patent WO9848046.
ACCESSION   A83807
VERSION     A83807.1  GI:6732985
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Pfeffer,K.
  TITLE     TAQMAN<TM>-PCR FOR THE DETECTION OF PATHOGENIC E. COLI STRAINS
  JOURNAL   Patent: WO 9848046-A 29-OCT-1998;
            BAVARIAN NORDIC RESEARCH INST (DE); PFEFFER KLAUS (DE)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        7 a      9 c      6 g      1 t
ORIGIN


  Query Match             73.3%;  Score 11;  DB 81;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+05;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 gcttgtgccgg 15
          ||||||||||||
Db     18 GCTTGTGCCGG 8


RESULT  11
AX015588/c
LOCUS       AX015588       18 bp    DNA             BCT       07-SEP-2000
DEFINITION  Sequence 15 from Patent WO9951723.
ACCESSION   AX015588
VERSION     AX015588.1  GI:10041426
KEYWORDS    .
SOURCE      Streptomyces mobaraensis.
  ORGANISM  Streptomyces mobaraensis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Dorsch,S., Otterbach,J., Pasternack,R., Dauscher,C.,
            Fuchsbauer,H.L., Mainusch,M. and Robenek,I.
  TITLE     Bacterial transglutaminases
  JOURNAL   Patent: WO 9951723-A 14-OCT-1999;
            DORSCH SIMONE (DE); OTTERBACH JENS (DE); PASTERNACK RALF (DE);
            DAUSCHER CHRISTINE (DE); FUCHSBAUER HANS LOTHAR (DE); MAINUSCH
            MARTINA (DE); ROBENEK ISABELLA (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Streptomyces mobaraensis"
                     /db_xref="taxon:35621"
BASE COUNT        3 a      6 c      9 g      0 t
ORIGIN


  Query Match             72.0%;  Score 10.8;  DB 2;  Length 18;
  Best Local Similarity   85.7%;  Pred. No. 3.3e+05;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      2 gtcgcttgtgccgg 15
          ||||||  ||||||
Db     15 GTCGCTGCTGCCGG 2


RESULT  12
E12143/c
LOCUS       E12143         19 bp    DNA             PAT       24-JUN-1998
DEFINITION  PCR primer for detecting Pseudomonas fluorescens.
ACCESSION   E12143
VERSION     E12143.1  GI:3250977
KEYWORDS    JP 1996256799-A/1.
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Murakami,K., Kudou,A., Yamada,H., Kanzaki,T. and Okada,K. .
  TITLE     ASSAY OF BACTERIUM IN SPECIMEN
  JOURNAL   Patent: JP 1996256799-A 1 08-OCT-1996;
            NISSHIN FLOUR MILLING CO LTD
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1996256799-A/1
            PD   08-OCT-1996
            PF   28-MAR-1995 JP 1995093259
            PI   MURAKAMI KOJI, KUDOU AKIKO, YAMADA HIDEAKI, KANZAKI TAKESHI,
            PI   OKADA KENZO
            PC   C12Q1/68,C12N15/09,C12Q1/06,G01N33/50,(C12Q1/68,C12R1:39); CC
             strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .19
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1...19
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        6 a      7 c      5 g      1 t
ORIGIN


  Query Match             72.0%;  Score 10.8;  DB 81;  Length 19;
  Best Local Similarity   85.7%;  Pred. No. 3.2e+05;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tgtcgcttgtgccg 14
          || |||||||||| |
Db     19 TGGCGCTTGTGCAG 6
```

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 23, 2001, 13:36:34 ; Search time 2149.74 Seconds
(without alignments)
26.187 Million cell updates/sec

Title: US-09-554-267-18
Perfect score: 11
Sequence: 1 ccccatggtgg 11

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1118133 seqs, 2558875100 residues

Total number of hits satisfying chosen parameters: 349344

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba1:*
2: gb_ba2:*
3: gb_om:*
4: gb_ov:*
5: gb_ph:*
6: gb_pl1:*
7: gb_pl2:*
8: gb_pr1:*
9: gb_pr2:*
10: gb_pr3:*
11: gb_ro:*
12: gb_sy:*
13: gb_un:*
14: em_fun:*
15: em_hum1:*
16: em_hum2:*
17: em_in:*
18: em_om:*
19: em_or:*
20: em_ov:*
21: em_pat:*
22: em_ph:*
23: em_pl:*
24: em_ro:*
25: em_sts:*
26: em_sy:*
27: em_un:*
28: em_vi:*
29: gb_ba3:*
30: gb_in1:*
31: gb_in2:*
32: gb_in3:*
33: gb_pl3:*
34: gb_pr4:*
35: em_ba1:*
36: em_ba2:*
37: em_htg1:*
38: em_htg2:*
39: em_htg3:*
40: em_htg4:*
41: em_htg5:*
42: em_htg6:*
43: em_htg7:*
44: em_htg8:*
45: em_htg9:*
46: em_htg10:*
47: em_hum3:*
48: em_hum4:*
49: em_hum5:*
50: em_hum6:*
51: gb_pr5:*
52: gb_pr6:*
53: gb_pr7:*
54: gb_htg1:*
55: gb_htg2:*
56: gb_htg3:*
57: gb_htg4:*
58: gb_htg5:*
59: gb_htg6:*
60: gb_htg7:*
61: gb_htg8:*
62: gb_htg9:*
63: gb_htg10:*
64: gb_htg11:*
65: gb_htg12:*
66: gb_htg13:*
67: gb_htg14:*
68: gb_htg15:*
69: gb_htg16:*
70: gb_htg17:*
71: gb_htg18:*
72: gb_htg19:*
73: gb_htg20:*
74: gb_htg21:*
75: gb_htg22:*
76: gb_htg23:*
77: gb_sts1:*
78: gb_sts2:*
79: gb_vi1:*
80: gb_vi2:*
81: gb_pat1:*
82: gb_pat2:*
83: em_htg0:*
84: gb_htg24:*
85: gb_pr8:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	11	100.0	11	13	AX022910	AX022910 Sequence
2	11	100.0	11	13	AX022929	AX022929 Sequence
3	11	100.0	11	13	AX022948	AX022948 Sequence
4	11	100.0	11	13	AX030498	AX030498 Sequence
5	11	100.0	11	13	AX030517	AX030517 Sequence
6	11	100.0	11	13	AX030536	AX030536 Sequence
C 7	11	100.0	12	81	A36015	A36015 Sequence 14
8	11	100.0	14	13	AX022896	AX022896 Sequence
9	11	100.0	14	13	AX022897	AX022897 Sequence
10	11	100.0	14	13	AX022915	AX022915 Sequence
11	11	100.0	14	13	AX022916	AX022916 Sequence
12	11	100.0	14	13	AX022934	AX022934 Sequence
13	11	100.0	14	13	AX022935	AX022935 Sequence
14	11	100.0	14	13	AX030484	AX030484 Sequence
15	11	100.0	14	13	AX030485	AX030485 Sequence
16	11	100.0	14	13	AX030503	AX030503 Sequence
17	11	100.0	14	13	AX030504	AX030504 Sequence
18	11	100.0	14	13	AX030522	AX030522 Sequence
19	11	100.0	14	13	AX030523	AX030523 Sequence
20	11	100.0	17	13	AX022895	AX022895 Sequence
21	11	100.0	17	13	AX022914	AX022914 Sequence

22	11	100.0	17	13	AX022933	AX022933 Sequence
23	11	100.0	17	13	AX030483	AX030483 Sequence
24	11	100.0	17	13	AX030502	AX030502 Sequence
25	11	100.0	17	13	AX030521	AX030521 Sequence
c 26	11	100.0	24	81	AR063265	AR063265 Sequence
27	11	100.0	24	85	S71212	S71212 PRNP=prion
c 28	11	100.0	27	81	I36339	I36339 Sequence 9
29	11	100.0	30	81	A50804	A50804 Sequence 25
30	11	100.0	31	81	I36340	I36340 Sequence 10
c 31	11	100.0	33	81	A36006	A36006 Sequence 5
c 32	11	100.0	36	12	AX019531	AX019531 Sequence
c 33	11	100.0	36	51	AX021210	AX021210 Sequence
c 34	11	100.0	36	81	A94277	A94277 Sequence 30
c 35	11	100.0	41	81	AR096921	AR096921 Sequence
c 36	11	100.0	41	81	AR096932	AR096932 Sequence
c 37	11	100.0	43	81	A56908	A56908 Sequence 4
38	11	100.0	45	81	AR055549	AR055549 Sequence
39	11	100.0	45	81	AR082733	AR082733 Sequence
40	11	100.0	45	81	AR084875	AR084875 Sequence
41	11	100.0	45	81	AR087683	AR087683 Sequence
42	11	100.0	45	81	AR094043	AR094043 Sequence
c 43	11	100.0	47	82	I84671	I84671 Sequence 5
c 44	10	90.9	20	81	AR085173	AR085173 Sequence
c 45	10	90.9	20	81	AR091863	AR091863 Sequence

ALIGNMENTS

```
RESULT   1
AX022910
LOCUS       AX022910       11 bp    DNA             UNA       07-SEP-2000
DEFINITION  Sequence 18 from Patent WO9925819.
ACCESSION   AX022910
VERSION     AX022910.1  GI:10046402
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Uhlmann,E., Weiser,C. and Peyman,A.
  TITLE     Antisense oligonucleotides against tenascin for treating vitiligo
  JOURNAL   Patent: WO 9925819-A 27-MAY-1999;
            UHLMANN EUGEN (DE); WEISER CAROLINE (DE); HOECHST MARION ROUSSEL DE
            GMBH (DE); PEYMAN ANUSCHIRWAN (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unidentified"
                     /db_xref="taxon:32644"
     exon            1. .11
BASE COUNT        1 a      4 c      4 g      2 t
ORIGIN


  Query Match             100.0%;  Score 11;  DB 13;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+04;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ccccatggtgg 11
          |||||||||||
Db      1 CCCCATGGTGG 11


RESULT   2
AX022929
LOCUS       AX022929       11 bp    DNA             UNA       07-SEP-2000
DEFINITION  Sequence 37 from Patent WO9925819.
ACCESSION   AX022929
VERSION     AX022929.1  GI:10046422
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Uhlmann,E., Weiser,C. and Peyman,A.
  TITLE     Antisense oligonucleotides against tenascin for treating vitiligo
  JOURNAL   Patent: WO 9925819-A 27-MAY-1999;
            UHLMANN EUGEN (DE); WEISER CAROLINE (DE); HOECHST MARION ROUSSEL DE
            GMBH (DE); PEYMAN ANUSCHIRWAN (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        1 a      4 c      4 g      2 t
ORIGIN


  Query Match             100.0%;  Score 11;  DB 13;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+04;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ccccatggtgg 11
          |||||||||||
Db      1 CCCCATGGTGG 11


RESULT   3
AX022948
LOCUS       AX022948       11 bp    DNA             UNA       07-SEP-2000
DEFINITION  Sequence 56 from Patent WO9925819.
ACCESSION   AX022948
VERSION     AX022948.1  GI:10046441
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Uhlmann,E., Weiser,C. and Peyman,A.
  TITLE     Antisense oligonucleotides against tenascin for treating vitiligo
  JOURNAL   Patent: WO 9925819-A 27-MAY-1999;
            UHLMANN EUGEN (DE); WEISER CAROLINE (DE); HOECHST MARION ROUSSEL DE
            GMBH (DE); PEYMAN ANUSCHIRWAN (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        1 a      4 c      4 g      2 t
ORIGIN


  Query Match             100.0%;  Score 11;  DB 13;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+04;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ccccatggtgg 11
          |||||||||||
Db      1 CCCCATGGTGG 11


RESULT   4
AX030498
LOCUS       AX030498       11 bp    DNA             UNA       20-SEP-2000
DEFINITION  Sequence 18 from Patent DE19750702.
ACCESSION   AX030498
VERSION     AX030498.1  GI:10278055
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Peyman,A.D., Uhlmann,E.D. and Weiser,C.D.
  TITLE     Antisense oligonucleotides that bind to sequences encoding human
            tenascin for treating depigmentation, cancer, inflammation and
            cardiovascular disease
  JOURNAL   Patent: DE 19750702-A 27-MAY-1999;
            HOECHST MARION ROUSSEL DE GMBH (DE)
```

```
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unidentified"
                     /db_xref="taxon:32644"
     exon            1. .11
BASE COUNT        1 a      4 c      4 g      2 t
ORIGIN


  Query Match             100.0%;  Score 11;  DB 13;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+04;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ccccatggtgg 11
          ||||||||||||
Db      1 CCCCATGGTGG 11


RESULT   5
AX030517
LOCUS       AX030517       11 bp    DNA             UNA       20-SEP-2000
DEFINITION  Sequence 37 from Patent DE19750702.
ACCESSION   AX030517
VERSION     AX030517.1  GI:10278074
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Peyman,A.D., Uhlmann,E.D. and Weiser,C.D.
  TITLE     Antisense oligonucleotides that bind to sequences encoding human
            tenascin for treating depigmentation, cancer, inflammation and
            cardiovascular disease
  JOURNAL   Patent: DE 19750702-A 27-MAY-1999;
            HOECHST MARION ROUSSEL DE GMBH (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        1 a      4 c      4 g      2 t
ORIGIN


  Query Match             100.0%;  Score 11;  DB 13;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+04;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ccccatggtgg 11
          ||||||||||||
Db      1 CCCCATGGTGG 11


RESULT   6
AX030536
LOCUS       AX030536       11 bp    DNA             UNA       20-SEP-2000
DEFINITION  Sequence 56 from Patent DE19750702.
ACCESSION   AX030536
VERSION     AX030536.1  GI:10278093
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Peyman,A.D., Uhlmann,E.D. and Weiser,C.D.
  TITLE     Antisense oligonucleotides that bind to sequences encoding human
            tenascin for treating depigmentation, cancer, inflammation and
            cardiovascular disease
  JOURNAL   Patent: DE 19750702-A 27-MAY-1999;
            HOECHST MARION ROUSSEL DE GMBH (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        1 a      4 c      4 g      2 t
ORIGIN


  Query Match             100.0%;  Score 11;  DB 13;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+04;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ccccatggtgg 11
          ||||||||||||
Db      1 CCCCATGGTGG 11


RESULT   7
A36015/c
LOCUS       A36015         12 bp    DNA             PAT       04-MAR-1997
DEFINITION  Sequence 14 from Patent EP0564801.
ACCESSION   A36015
VERSION     A36015.1  GI:2293643
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Sommergruber,W.D., Auer,H., Blaas,D.D., Frasel,L., Hartmuth,K.D.,
            Kuechler,E.P., Kowalski,H., Liebig,H.D., Skern,T.D. and
            Ziegler,G.S.
  TITLE     Analysis of host cell shut-off
  JOURNAL   Patent: EP 0564801-A 14 13-OCT-1993;
            BOEHRINGER INGELHEIM INT (DE)
COMMENT     Other publication DE 4206769 930909
            Other publication JP 6197799 940719
            Other publication CA 2090834 930905
            Other publication DE 4217929 931202.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        3 a      4 c      4 g      1 t
ORIGIN


  Query Match             100.0%;  Score 11;  DB 81;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+04;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ccccatggtgg 11
          ||||||||||||
Db     12 CCCCATGGTGG 2


RESULT   8
AX022896
LOCUS       AX022896       14 bp    DNA             UNA       07-SEP-2000
DEFINITION  Sequence 4 from Patent WO9925819.
ACCESSION   AX022896
VERSION     AX022896.1  GI:10046387
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Uhlmann,E., Weiser,C. and Peyman,A.
  TITLE     Antisense oligonucleotides against tenascin for treating vitiligo
  JOURNAL   Patent: WO 9925819-A 27-MAY-1999;
            UHLMANN EUGEN (DE); WEISER CAROLINE (DE); HOECHST MARION ROUSSEL DE
            GMBH (DE); PEYMAN ANUSCHIRWAN (DE)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unidentified"
                     /db_xref="taxon:32644"
     exon            1. .14
BASE COUNT        1 a      5 c      6 g      2 t
```

```
ORIGIN


  Query Match             100.0%;  Score 11;  DB 13;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2e+04;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ccccatggtgg 11
          ||||||||||||
Db      4 CCCCATGGTGG 14


RESULT   9
AX022897
LOCUS       AX022897       14 bp    DNA             UNA       07-SEP-2000
DEFINITION  Sequence 5 from Patent WO9925819.
ACCESSION   AX022897
VERSION     AX022897.1  GI:10046388
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Uhlmann,E., Weiser,C. and Peyman,A.
  TITLE     Antisense oligonucleotides against tenascin for treating vitiligo
  JOURNAL   Patent: WO 9925819-A 27-MAY-1999;
            UHLMANN EUGEN (DE); WEISER CAROLINE (DE); HOECHST MARION ROUSSEL DE
            GMBH (DE); PEYMAN ANUSCHIRWAN (DE)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unidentified"
                     /db_xref="taxon:32644"
     exon            1. .14
BASE COUNT        2 a      4 c      6 g      2 t
ORIGIN


  Query Match             100.0%;  Score 11;  DB 13;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2e+04;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ccccatggtgg 11
          ||||||||||||
Db      1 CCCCATGGTGG 11


RESULT  10
AX022915
LOCUS       AX022915       14 bp    DNA             UNA       07-SEP-2000
DEFINITION  Sequence 23 from Patent WO9925819.
ACCESSION   AX022915
VERSION     AX022915.1  GI:10046407
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Uhlmann,E., Weiser,C. and Peyman,A.
  TITLE     Antisense oligonucleotides against tenascin for treating vitiligo
  JOURNAL   Patent: WO 9925819-A 27-MAY-1999;
            UHLMANN EUGEN (DE); WEISER CAROLINE (DE); HOECHST MARION ROUSSEL DE
            GMBH (DE); PEYMAN ANUSCHIRWAN (DE)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        1 a      5 c      6 g      2 t
ORIGIN


  Query Match             100.0%;  Score 11;  DB 13;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2e+04;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ccccatggtgg 11
          ||||||||||||
Db      4 CCCCATGGTGG 14


RESULT  11
AX022916
LOCUS       AX022916       14 bp    DNA             UNA       07-SEP-2000
DEFINITION  Sequence 24 from Patent WO9925819.
ACCESSION   AX022916
VERSION     AX022916.1  GI:10046408
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Uhlmann,E., Weiser,C. and Peyman,A.
  TITLE     Antisense oligonucleotides against tenascin for treating vitiligo
  JOURNAL   Patent: WO 9925819-A 27-MAY-1999;
            UHLMANN EUGEN (DE); WEISER CAROLINE (DE); HOECHST MARION ROUSSEL DE
            GMBH (DE); PEYMAN ANUSCHIRWAN (DE)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        2 a      4 c      6 g      2 t
ORIGIN


  Query Match             100.0%;  Score 11;  DB 13;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2e+04;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ccccatggtgg 11
          ||||||||||||
Db      1 CCCCATGGTGG 11


RESULT  12
AX022934
LOCUS       AX022934       14 bp    DNA             UNA       07-SEP-2000
DEFINITION  Sequence 42 from Patent WO9925819.
ACCESSION   AX022934
VERSION     AX022934.1  GI:10046427
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Uhlmann,E., Weiser,C. and Peyman,A.
  TITLE     Antisense oligonucleotides against tenascin for treating vitiligo
  JOURNAL   Patent: WO 9925819-A 27-MAY-1999;
            UHLMANN EUGEN (DE); WEISER CAROLINE (DE); HOECHST MARION ROUSSEL DE
            GMBH (DE); PEYMAN ANUSCHIRWAN (DE)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        1 a      5 c      6 g      2 t
ORIGIN


  Query Match             100.0%;  Score 11;  DB 13;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2e+04;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ccccatggtgg 11
          ||||||||||||
Db      4 CCCCATGGTGG 14


RESULT  13
```

```
AX022935
LOCUS       AX022935       14 bp    DNA             UNA       07-SEP-2000
DEFINITION  Sequence 43 from Patent WO9925819.
ACCESSION   AX022935
VERSION     AX022935.1  GI:10046428
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Uhlmann,E., Weiser,C. and Peyman,A.
  TITLE     Antisense oligonucleotides against tenascin for treating vitiligo
  JOURNAL   Patent: WO 9925819-A 27-MAY-1999;
            UHLMANN EUGEN (DE); WEISER CAROLINE (DE); HOECHST MARION ROUSSEL DE
            GMBH (DE); PEYMAN ANUSCHIRWAN (DE)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        2 a      4 c      6 g      2 t
ORIGIN


  Query Match            100.0%;  Score 11;  DB 13;  Length 14;
  Best Local Similarity  100.0%;  Pred. No. 2e+04;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ccccatggtgg 11
          ||||||||||||
Db      1 CCCCATGGTGG 11


RESULT  14
AX030484
LOCUS       AX030484       14 bp    DNA             UNA       20-SEP-2000
DEFINITION  Sequence 4 from Patent DE19750702.
ACCESSION   AX030484
VERSION     AX030484.1  GI:10278041
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Peyman,A.D., Uhlmann,E.D. and Weiser,C.D.
  TITLE     Antisense oligonucleotides that bind to sequences encoding human
            tenascin for treating depigmentation, cancer, inflammation and
            cardiovascular disease
  JOURNAL   Patent: DE 19750702-A 27-MAY-1999;
            HOECHST MARION ROUSSEL DE GMBH (DE)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unidentified"
                     /db_xref="taxon:32644"
     exon            1. .14
BASE COUNT        1 a      5 c      6 g      2 t
ORIGIN


  Query Match            100.0%;  Score 11;  DB 13;  Length 14;
  Best Local Similarity  100.0%;  Pred. No. 2e+04;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ccccatggtgg 11
          ||||||||||||
Db      4 CCCCATGGTGG 14


RESULT  15
AX030485
LOCUS       AX030485       14 bp    DNA             UNA       20-SEP-2000
DEFINITION  Sequence 5 from Patent DE19750702.
ACCESSION   AX030485
VERSION     AX030485.1  GI:10278042
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Peyman,A.D., Uhlmann,E.D. and Weiser,C.D.
  TITLE     Antisense oligonucleotides that bind to sequences encoding human
            tenascin for treating depigmentation, cancer, inflammation and
            cardiovascular disease
  JOURNAL   Patent: DE 19750702-A 27-MAY-1999;
            HOECHST MARION ROUSSEL DE GMBH (DE)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unidentified"
                     /db_xref="taxon:32644"
     exon            1. .14
BASE COUNT        2 a      4 c      6 g      2 t
ORIGIN


  Query Match            100.0%;  Score 11;  DB 13;  Length 14;
  Best Local Similarity  100.0%;  Pred. No. 2e+04;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ccccatggtgg 11
          ||||||||||||
Db      1 CCCCATGGTGG 11


Search completed: March 23, 2001, 13:36:34
Job time: 27637 sec
```

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 23, 2001, 16:04:40 ; Search time 551.33 Seconds
(without alignments)
7.495 Million cell updates/sec

Title: US-09-554-267-18
Perfect score: 11
Sequence: 1 ccccatggtgg 11

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 624296

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_36:*
1: /cgn2_2/gcgdata/geneseq/geneseqn/NA1980.DAT:*
2: /cgn2_2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
3: /cgn2_2/gcgdata/geneseq/geneseqn/NA1982.DAT:*
4: /cgn2_2/gcgdata/geneseq/geneseqn/NA1983.DAT:*
5: /cgn2_2/gcgdata/geneseq/geneseqn/NA1984.DAT:*
6: /cgn2_2/gcgdata/geneseq/geneseqn/NA1985.DAT:*
7: /cgn2_2/gcgdata/geneseq/geneseqn/NA1986.DAT:*
8: /cgn2_2/gcgdata/geneseq/geneseqn/NA1987.DAT:*
9: /cgn2_2/gcgdata/geneseq/geneseqn/NA1988.DAT:*
10: /cgn2_2/gcgdata/geneseq/geneseqn/NA1989.DAT:*
11: /cgn2_2/gcgdata/geneseq/geneseqn/NA1990.DAT:*
12: /cgn2_2/gcgdata/geneseq/geneseqn/NA1991.DAT:*
13: /cgn2_2/gcgdata/geneseq/geneseqn/NA1992.DAT:*
14: /cgn2_2/gcgdata/geneseq/geneseqn/NA1993.DAT:*
15: /cgn2_2/gcgdata/geneseq/geneseqn/NA1994.DAT:*
16: /cgn2_2/gcgdata/geneseq/geneseqn/NA1995.DAT:*
17: /cgn2_2/gcgdata/geneseq/geneseqn/NA1996.DAT:*
18: /cgn2_2/gcgdata/geneseq/geneseqn/NA1997.DAT:*
19: /cgn2_2/gcgdata/geneseq/geneseqn/NA1998.DAT:*
20: /cgn2_2/gcgdata/geneseq/geneseqn/NA1999.DAT:*
21: /cgn2_2/gcgdata/geneseq/geneseqn/NA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		11	100.0	18	15	Q77634	Ribonucleotide to
c 2		11	100.0	18	15	Q77620	Antisense polynucl
c 3		11	100.0	18	15	Q77648	Antisense ribonucl
4		11	100.0	18	15	Q76393	Polynucleotide to
5		11	100.0	24	15	Q77617	Polynucleotide to
c 6		11	100.0	24	15	Q77659	Antisense ribonucl
c 7		11	100.0	24	15	Q77631	Antisense polynucl
8		11	100.0	24	15	Q77645	Ribonucleotide to
c 9		11	100.0	24	21	Z61427	PCR primer for DNA
c	10	11	100.0	27	18	T90893	5' primer for epid
c	11	11	100.0	30	19	V24270	Chimeric antibody
c	12	11	100.0	30	20	X00114	Human antibody PCR
c	13	11	100.0	30	21	Z58895	PCR primer MBC1HVS
c	14	11	100.0	31	18	T68725	Human osteo antivi
c	15	11	100.0	31	19	V45332	Human extracellula
c	16	11	100.0	31	21	Z58151	Human FAST-1 gene
c	17	11	100.0	34	17	T10560	Serum paraoxonase
c	18	11	100.0	35	19	V28946	Plasmid pAMG21 dN2
c	19	11	100.0	35	19	V28940	Plasmid pAMG21 dN2
c	20	11	100.0	35	19	V28942	Plasmid pAMG21 dN2
c	21	11	100.0	35	19	V28944	Plasmid pAMG21 dN2
c	22	11	100.0	35	19	V11789	Plasmiid pAMG21 Hi
c	23	11	100.0	35	19	V11793	Plasmid pAMG21 hFG
c	24	11	100.0	35	20	X36573	PCR primer for hum
c	25	11	100.0	36	15	Q76387	Tenascin gene cons
26		11	100.0	36	15	Q76386	Tenascin gene cons
c	27	11	100.0	36	15	Q77661	Tenascin gene mRNA
28		11	100.0	36	15	Q77662	Tenascin gene mRNA
c	29	11	100.0	36	19	V24252	Chimeric antibody
c	30	11	100.0	36	20	X87664	Macrophage stimula
c	31	11	100.0	36	20	X00096	Mouse humanised an
c	32	11	100.0	36	21	Z58877	PCR primer MBC1HVS
c	33	11	100.0	36	21	Z36161	PCR primer HCPr59
c	34	11	100.0	38	20	X60345	Sense PCR primer u
c	35	11	100.0	40	16	Q88332	Maize alpha-tubuli
c	36	11	100.0	41	18	T97210	Kappa chain variab
c	37	11	100.0	41	18	T97199	Heavy chain primer
c	38	11	100.0	42	21	Z95273	Monkey erythropoie
c	39	11	100.0	43	17	T42077	Human erythropoiet
40		11	100.0	45	20	Z22742	Oligo 2 for immuni
41		11	100.0	45	20	V64819	Zona pellucida ZP
42		11	100.0	45	21	Z95679	Recombinant ZPC ve
43		11	100.0	45	21	Z46287	Expression vector
44		11	100.0	45	21	Z33276	Recombinant ZPC ve
45		11	100.0	45	21	Z37826	Oligonucleotide #2

ALIGNMENTS

RESULT 1
Q77634
ID Q77634 standard; RNA; 18 BP.
XX
AC Q77634;
XX
DT 02-JUN-1995 (first entry)
XX
DE Ribonucleotide to tenascin gene consensus mRNA initiation site -9-+9.
XX
KW Antisense; polynucleotide; sense strand; tenascin; complementary;
KW consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW proliferation; growth stimulatory; transcription; vascular stenosis;
KW post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW organ transplant; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_difference 1..18
FT /*tag= a
FT /note= "phosphodiester bonds between nucleotides
FT may be replaced by phosphorothioate bonds"
XX
PN WO9421664-A.
XX
PD 29-SEP-1994.
XX
PF 24-MAR-1994; 94WO-US03206.
XX
PR 25-MAR-1993; 93US-0037025.
XX
PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI Denner LA, Dixon RAF, Rege AA, Stacy DL;

XX
DR WPI; 1994-316926/39.
XX
PT Synthetic anti-sense polynucleotide - hybridises to tenascin
PT gene, useful for inhibiting vascular smooth muscle cell
PT proliferation.
XX
PS Claim 5; Page 47; 64pp; English.
XX
CC A series of polynucleotides, either DNA (Q76388 and Q76392-400 and
CC Q77614-18) or RNA (Q76390 and Q77633-46), directed against the consensus
CC mRNA initiation site sequence (Q77661) for the tenascin gene. The
CC polynucleotides are based on the degenerate sequence (Q76386) of the
CC tenascin gene. Tenascin is an extracellular matrix glycoprotein
CC consisting six disulphide-linked subunits, each having molecular mass of
CC 190-250 kDa. Tenascin may be important for smooth muscle cell
CC proliferation as the protein has growth stimulatory activity. The
CC polynucleotides can be used to inhibit transcription of the gene or
CC translation of the mRNA encoding tenascin. The method is applicable to a
CC number of diseases where the proliferation of smooth muscle is involved
CC e.g. vascular stenosis, post-angioplasty restenosis and other
CC non-angioplasty procedures such as cardiac hypertrophy, vascular surgery
CC and organ transplant.
XX
SQ Sequence 18 BP; 2 A; 5 C; 8 G; 3 U; 0 other;

Query Match 100.0%; Score 11; DB 15; Length 18;
Best Local Similarity 81.8%; Pred. No. 4.7e+02;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ccccatggtgg 11
|||||:||:||
Db 4 ccccauggugg 14

RESULT 2
Q77620/c
ID Q77620 standard; DNA; 18 BP.
XX
AC Q77620;
XX
DT 01-JUN-1995 (first entry)
XX
DE Antisense polynucleotide binds to tenascin gene consensus at -9-+9.
XX
KW Antisense; polynucleotide; sense strand; tenascin; complementary;
KW consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW proliferation; growth stimulatory; transcription; vascular stenosis;
KW post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW organ transplant; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_difference 1..18
FT /*tag= a
FT /note= "phosphodiester bonds between nucleotides
FT may be replaced by phosphorothioate bonds"
XX
PN WO9421664-A.
XX
PD 29-SEP-1994.
XX
PF 24-MAR-1994; 94WO-US03206.
XX
PR 25-MAR-1993; 93US-0037025.
XX
PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI Denner LA, Dixon RAF, Rege AA, Stacy DL;
XX
DR WPI; 1994-316926/39.
XX
PT Synthetic anti-sense polynucleotide - hybridises to tenascin
PT gene, useful for inhibiting vascular smooth muscle cell
PT proliferation.
XX
PS Claim 10; Page 44; 64pp; English.
XX
CC A series of antisense polynucleotides, either DNA (Q76388 and Q77619-32)
CC or RNA (Q76390 and Q77647-60) directed against the sense strand of the
CC gene encoding tenascin. The polynucleotides are based on the
CC complementary sequence (Q76386) of the consensus mRNA initiation site
CC sequence (Q77661) for the tenascin gene. Tenascin is an extracellular
CC matrix glycoprotein consisting six disulphide-linked subunits, each
CC having molecular mass of 190-250 kDa. Tenascin may be important for
CC smooth muscle cell proliferation as the protein has growth stimulatory
CC activity. The polynucleotides can be used to inhibit transcription
CC of the gene or translation of the mRNA encoding tenascin. The method is
CC applicable to a number of diseases where the proliferation of smooth
CC muscle is involved e.g. vascular stenosis, post-angioplasty restenosis
CC and other non-angioplasty procedures such as cardiac hypertrophy,
CC vascular surgery and organ transplant.
XX
SQ Sequence 18 BP; 3 A; 8 C; 5 G; 2 T; 0 other;

Query Match 100.0%; Score 11; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ccccatggtgg 11
||||||||||||
Db 15 CCCCATGGTGG 5

RESULT 3
Q77648/c
ID Q77648 standard; RNA; 18 BP.
XX
AC Q77648;
XX
DT 02-JUN-1995 (first entry)
XX
DE Antisense ribonucleotide binds to tenascin gene consensus at -9-+9.
XX
KW Antisense; polynucleotide; sense strand; tenascin; complementary;
KW consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW proliferation; growth stimulatory; transcription; vascular stenosis;
KW post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW organ transplant; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_difference 1..18
FT /*tag= a
FT /note= "phosphodiester bonds between nucleotides
FT may be replaced by phosphorothioate bonds"
XX
PN WO9421664-A.
XX
PD 29-SEP-1994.
XX
PF 24-MAR-1994; 94WO-US03206.
XX
PR 25-MAR-1993; 93US-0037025.
XX
PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI Denner LA, Dixon RAF, Rege AA, Stacy DL;
XX
DR WPI; 1994-316926/39.
XX
PT Synthetic anti-sense polynucleotide - hybridises to tenascin

```
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 10; Page 51; 64pp; English.
XX
CC   A series of antisense polynucleotides, either DNA (Q76388 and Q77619-32)
CC   or RNA (Q76390 and Q77647-60) directed against the sense strand of the
CC   gene encoding tenascin.  The polynucleotides are based on the
CC   complementary sequence (Q76386) of the consensus mRNA initiation site
CC   sequence (Q77661) for the tenascin gene.  Tenascin is an extracellular
CC   matrix glycoprotein consisting six disulphide-linked subunits, each
CC   having molecular mass of 190-250 kDa.  Tenascin may be important for
CC   smooth muscle cell proliferation as the protein has growth stimulatory
CC   activity.  The polynucleotides can be used to inhibit transcription
CC   of the gene or translation of the mRNA encoding tenascin.  The method is
CC   applicable to a number of diseases where the proliferation of smooth
CC   muscle is involved e.g. vascular stenosis, post-angioplasty restenosis
CC   and other non-angioplasty procedures such as cardiac hypertrophy,
CC   vascular surgery and organ transplant.
XX
SQ   Sequence 18 BP; 3 A; 8 C; 5 G; 2 U; 0 other;


  Query Match             100.0%;  Score 11;  DB 15;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ccccatggtgg 11
           ||||||||||| |
Db      15 CCCCATGGTGG 5


RESULT   4
Q76393
ID   Q76393 standard; DNA; 18 BP.
XX
AC   Q76393;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Polynucleotide to tenascin gene consensus mRNA initiation site -9-+9.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..18
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                          may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 5; Page 40; 64pp; English.
XX
CC   A series of polynucleotides, either DNA (Q76388 and Q76392-400 and
CC   Q77614-18) or RNA (Q76390 and Q77633-46), directed against the ccnsensus
CC   mRNA initiation site sequence (Q77661) for the tenascin gene.  The
CC   polynucleotides are based on the degenerate sequence (Q76386) of the
CC   tenascin gene.  Tenascin is an extracellular matrix glycoprotein
CC   consisting six disulphide-linked subunits, each having molecular mass of
CC   190-250 kDa.  Tenascin may be important for smooth muscle cell
CC   proliferation as the protein has growth stimulatory activity.  The
CC   polynucleotides can be used to inhibit transcription of the gene or
CC   translation of the mRNA encoding tenascin. The method is applicable to a
CC   number of diseases where the proliferation of smooth muscle is involved
CC   e.g. vascular stenosis, post-angioplasty restenosis and other
CC   non-angioplasty procedures such as cardiac hypertrophy, vascular surgery
CC   and organ transplant.
XX
SQ   Sequence 18 BP; 2 A; 5 C; 8 G; 3 T; 0 other;


  Query Match             100.0%;  Score 11;  DB 15;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ccccatggtgg 11
           ||||||||||| |
Db       4 ccccatggtgg 14


RESULT   5
Q77617
ID   Q77617 standard; DNA; 24 BP.
XX
AC   Q77617;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Polynucleotide to tenascin gene consensus mRNA initiation site -6-+18.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..24
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                          may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 5; Page 43; 64pp; English.
```

```
XX
CC   A series of polynucleotides, either DNA (Q76388 and Q76392-400 and
CC   Q77614-18) or RNA (Q76390 and Q77633-46), directed against the consensus
CC   mRNA initiation site sequence (Q77661) for the tenascin gene.  The
CC   polynucleotides are based on the degenerate sequence (Q76386) of the
CC   tenascin gene.  Tenascin is an extracellular matrix glycoprotein
CC   consisting six disulphide-linked subunits, each having molecular mass of
CC   190-250 kDa.  Tenascin may be important for smooth muscle cell
CC   proliferation as the protein has growth stimulatory activity.  The
CC   polynucleotides can be used to inhibit transcription of the gene or
CC   translation of the mRNA encoding tenascin. The method is applicable to a
CC   number of diseases where the proliferation of smooth muscle is involved
CC   e.g. vascular stenosis, post-angioplasty restenosis and other
CC   non-angioplasty procedures such as cardiac hypertrophy, vascular surgery
CC   and organ transplant.
XX
SQ   Sequence 24 BP; 4 A; 7 C; 8 G; 5 T; 0 other;


  Query Match             100.0%;  Score 11;  DB 15;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ccccatggtgg 11
          ||||||||||| |
Db     13 ccccatggtgg 23


RESULT   6
Q77659/c
ID   Q77659 standard; RNA; 24 BP.
XX
AC   Q77659;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Antisense ribonucleotide binds to tenascin gene consensus at -6-+18.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..24
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                          may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 10; Page 53; 64pp; English.
XX
CC   A series of antisense polynucleotides, either DNA (Q76388 and Q77619-32)
CC   or RNA (Q76390 and Q77647-60) directed against the sense strand of the
CC   gene encoding tenascin.  The polynucleotides are based on the
CC   complementary sequence (Q76386) of the consensus mRNA initiation site
CC   sequence (Q77661) for the tenascin gene.  Tenascin is an extracellular
CC   matrix glycoprotein consisting six disulphide-linked subunits, each
CC   having molecular mass of 190-250 kDa.  Tenascin may be important for
CC   smooth muscle cell proliferation as the protein has growth stimulatory
CC   activity.  The polynucleotides can be used to inhibit transcription
CC   of the gene or translation of the mRNA encoding tenascin.  The method is
CC   applicable to a number of diseases where the proliferation of smooth
CC   muscle is involved e.g. vascular stenosis, post-angioplasty restenosis
CC   and other non-angioplasty procedures such as cardiac hypertrophy,
CC   vascular surgery and organ transplant.
XX
SQ   Sequence 24 BP; 5 A; 8 C; 7 G; 4 U; 0 other;


  Query Match             100.0%;  Score 11;  DB 15;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ccccatggtgg 11
          ||||||||||| |
Db     12 CCCCATGGTGG 2


RESULT   7
Q77631/c
ID   Q77631 standard; DNA; 24 BP.
XX
AC   Q77631;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Antisense polynucleotide binds to tenascin gene consensus at -6-+18.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..24
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                          may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 10; Page 46; 64pp; English.
XX
CC   A series of antisense polynucleotides, either DNA (Q76388 and Q77619-32)
CC   or RNA (Q76390 and Q77647-60) directed against the sense strand of the
CC   gene encoding tenascin.  The polynucleotides are based on the
```

```
CC   complementary sequence (Q76386) of the consensus mRNA initiation site
CC   sequence (Q77661) for the tenascin gene.  Tenascin is an extracellular
CC   matrix glycoprotein consisting six disulphide-linked subunits, each
CC   having molecular mass of 190-250 kDa.  Tenascin may be important for
CC   smooth muscle cell proliferation as the protein has growth stimulatory
CC   activity.  The polynucleotides can be used to inhibit transcription
CC   of the gene or translation of the mRNA encoding tenascin.  The method is
CC   applicable to a number of diseases where the proliferation of smooth
CC   muscle is involved e.g. vascular stenosis, post-angioplasty restenosis
CC   and other non-angioplasty procedures such as cardiac hypertrophy,
CC   vascular surgery and organ transplant.
XX
SQ   Sequence 24 BP; 5 A; 8 C; 7 G; 4 T; 0 other;

  Query Match             100.0%;  Score 11;  DB 15;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ccccatggtgg 11
          ||||||||||||
Db     12 CCCCATGGTGG 2


RESULT   8
Q77645
ID   Q77645 standard; RNA; 24 BP.
XX
AC   Q77645;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Ribonucleotide to tenascin gene consensus mRNA initiation site -6-+18.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..24
FT                   /*tag= a
FT                   /note= "phosphodiester bonds between nucleotides
FT                          may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 5; Page 50; 64pp; English.
XX
CC   A series of polynucleotides, either DNA (Q76388 and Q76392-400 and
CC   Q77614-18) or RNA (Q76390 and Q77633-46), directed against the consensus
CC   mRNA initiation site sequence (Q77661) for the tenascin gene.  The
CC   polynucleotides are based on the degenerate sequence (Q76386) of the
CC   tenascin gene.  Tenascin is an extracellular matrix glycoprotein
CC   consisting six disulphide-linked subunits, each having molecular mass of
CC   190-250 kDa.  Tenascin may be important for smooth muscle cell
CC   proliferation as the protein has growth stimulatory activity.  The
CC   polynucleotides can be used to inhibit transcription of the gene or
CC   translation of the mRNA encoding tenascin. The method is applicable to a
CC   number of diseases where the proliferation of smooth muscle is involved
CC   e.g. vascular stenosis, post-angioplasty restenosis and other
CC   non-angioplasty procedures such as cardiac hypertrophy, vascular surgery
CC   and organ transplant.
XX
SQ   Sequence 24 BP; 4 A; 7 C; 8 G; 5 U; 0 other;

  Query Match             100.0%;  Score 11;  DB 15;  Length 24;
  Best Local Similarity   81.8%;  Pred. No. 4.8e+02;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ccccatggtgg 11
          |||||:||:||
Db     13 ccccauggugg 23


RESULT   9
Z61427/c
ID   Z61427 standard; DNA; 24 BP.
XX
AC   Z61427;
XX
DT   19-JUN-2000  (first entry)
XX
DE   PCR primer for DNA encoding short extracellular form of human B7-1.
XX
KW   Short form; B7-1; CD80; T-cell costimulator; antigen presenting cell;
KW   CD28; CTLA4; T cell surface receptor; cytokine production;
KW   cell proliferation; T cell; infection; autoimmune disease; inflammation;
KW   quality assurance; cancer; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200008057-A2.
XX
PD   17-FEB-2000.
XX
PF   05-AUG-1999;   99WO-US17906.
XX
PR   07-AUG-1998;   98US-0095663.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Baum PR;
XX
DR   WPI; 2000-205674/18.
XX
PT   Novel B7L-1 polypeptide and nucleotides encoding them useful as T cell
PT   costimulatory molecules for therapeutics against infections, autoimmune
PT   diseases and inflammation
XX
PS   Example 4; Page 50; 57pp; English.
XX
CC   PCR primers Z61426-28 were used to amplify DNA encoding the short
CC   extracellular form of human B7-1 (CD80). B7-1 is a T-cell
CC   costimulatory molecule that is found on the surface of antigen
CC   presenting cells (APCs). CD28 and CTLA4 are its T cell surface
CC   receptors. B7-1 interacts with CD28 to signal cytokine production,
CC   cell proliferation, and the generation of effector and memory T cells.
CC   Disorders mediated by interaction of B7-1 and its binding partner,
CC   such as infections, autoimmune diseases and inflammation, are treated
CC   by administering B7L-1 to the disordered mammal. B7L-1 polypeptides
CC   are useful to separate cells expressing a protein to which it binds
CC   and to measure the biological activity of LDCAM polypeptides. They can
CC   also be used as reagents for conducting quality assurance studies e.g.,
CC   to monitor shelf life and stability of proteins to which it binds, and
CC   as carriers for delivering agents attached to cells bearing its counter
```

```
CC   structure, LDCAM or other cell receptors. They are also useful as a
CC   research tool for studying T-cell signalling and proliferation. They are
CC   employed in in vitro assays for detecting interactions of LDCAM with
CC   T-cell receptors. Diagnostic and therapeutic agents, such as drugs,
CC   toxins, radionuclides, chromophores, and enzymes which catalyse a
CC   colorimetric or fluorometric reaction, may be attached to a B7L-1
CC   polypeptide, e.g. nitrogen mustards are attached to the B7L-1
CC   and used to treat various forms of cancer.
XX
SQ   Sequence 24 BP; 5 A; 7 C; 8 G; 4 T; 0 other;


  Query Match             100.0%;  Score 11;  DB 21;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ccccatggtgg 11
          ||||||||||||
Db     22 CCCCATGGTGG 12


RESULT  10
T90893/c
ID   T90893 standard; DNA; 27 BP.
XX
AC   T90893;
XX
DT   22-APR-1998  (first entry)
XX
DE   5' primer for epidermal differentiation factor coding sequence.
XX
KW   Epidermal differentiation factor; human; EDF; therapy; skin disorder;
KW   haematopoietic cell growth; pruritus; dermatitis; hair follicle disorder;
KW   bacterial skin infection; superficial fungal infection; sebaceous gland;
KW   scaling papular disease; inflammatory skin reaction; bullous disease;
KW   pigmentary disorder; skin tumour; bone formation promoter; osteoporosis;
KW   osteogenesis imperfecta; osteodystrophy; osteohypertrophy; osteopetrosis;
KW   osteoma; osteoblastoma; PCR primer; amplify; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9735976-A2.
XX
PD   02-OCT-1997.
XX
PF   27-MAR-1997;   97WO-US04962.
XX
PR   12-MAR-1997;   97US-0815718.
PR   27-MAR-1996;   96US-0014220.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Dillon PJ,  Gentz RL,  Li H,  Ni J;
XX
DR   WPI; 1997-489639/45.
XX
PT   New isolated epidermal differentiation factor - used to develop
PT   products for e.g. stimulating haematopoietic cell growth or for
PT   treating skin or bone disorders
XX
PS   Example 2; Page 33-34; 51pp; English.
XX
CC   This sequence represents a primer for the human epidermal differentiation
CC   factor (EDF) coding sequence of the invention (see T90890). The EDF
CC   protein encoded by the amplified sequence can be used to develop products
CC   for diagnosis and therapy of diseases resulting from altered EDF
CC   expression. The protein can be used e.g. to stimulate haematopoietic cell
CC   growth, to treat or prevent skin disorders such as pruritus, dermatitis,
CC   bacterial skin infections, superficial fungal infections; parasitic skin
CC   infections, viral skin infections, disorders of hair follicles and
CC   sebaceous glands, scaling papular diseases, inflammatory skin reactions,
CC   bullous diseases, disorders of cornification, pigmentary disorders,
CC   disorders of sweating, or skin tumours or to promote bone formation for
CC   healing of bone fractures and treatment of osteoporosis and osteogenesis
CC   imperfecta. Antagonists of the EDF protein can be used for treating
CC   e.g. osteodystrophy, osteohypertrophy, osteoma, osteopetrosis,
CC   osteoporosis or osteoblastoma.
XX
SQ   Sequence 27 BP; 6 A; 11 C; 8 G; 2 T; 0 other;


  Query Match             100.0%;  Score 11;  DB 18;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ccccatggtgg 11
          ||||||||||||
Db     18 CCCCATGGTGG 8


RESULT  11
V24270/c
ID   V24270 standard; DNA; 30 BP.
XX
AC   V24270;
XX
DT   03-SEP-1998  (first entry)
XX
DE   Chimeric antibody against hPTRP human H chain PCR primer MBC1HVS1.
XX
KW   Chimeric; antibody; human parathormone related peptide; hPTRP; mouse;
KW   L chain; H chain; hypercalcaemia; cancer; malignant lymphoma; CDR;
KW   hypophosphaemia; pathogen; vitamin D resistance; V region; C region;
KW   humanised; PCR primer ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9813388-A1.
XX
PD   02-APR-1998.
XX
PF   24-SEP-1997;   97WO-JP03382.
XX
PR   24-JUL-1997;   97JP-0214168.
PR   26-SEP-1996;   96JP-0255196.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
PI   Sato K,  Wakahara Y,  Yabuta N;
XX
DR   WPI; 1998-230640/20.
XX
PT   New chimeric antibodies against human parathormone related
PT   peptide(s) - useful for, e.g. treatment of hypercalcaemia and other
PT   disorders caused by malignant neoplasm(s)
XX
PS   Example 3; Page 105; 182pp; Japanese.
XX
CC   New antibodies have been developed which are specific for human
CC   parathormone related peptides (hPTRP). The antibodies comprise chimeric
CC   L and/or H chains, where the C region is of human and L region of mouse,
CC   origin. The present sequence represents a PCR primer used in an example
CC   of the present invention. Host cells, transformed with vectors
CC   containing DNA encoding antibodies of the invention, can be used to
CC   produce the antibodies. The antibodies may be used to treat
CC   hypercalcaemia, especially that due to a malignancy, e.g. cancers of
CC   pancreas, lung, throat, larynx, tongue, gum, oesophagus, stomach, liver,
CC   breast, kidney, bladder, womb or prostate or malignant lymphoma. They
CC   may also be used for treatment of hypophosphaemia such as that due to
CC   pathogens or to vitamin D resistance.
XX
SQ   Sequence 30 BP; 4 A; 7 C; 10 G; 9 T; 0 other;
```

```
  Query Match             100.0%;  Score 11;  DB 19;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ccccatggtgg 11
           ||||||||||||
Db      21 CCCCATGGTGG 11


RESULT  12
X00114/c
ID   X00114 standard; DNA; 30 BP.
XX
AC   X00114;
XX
DT   14-APR-1999  (first entry)
XX
DE   Human antibody PCR primer MBC1HVS1.
XX
KW   Human; parathyroid hormone related protein; PTHrP; cachexia; cancer;
KW   inhibitor; humanised; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9851329-A1.
XX
PD   19-NOV-1998.
XX
PF   13-MAY-1998;   98WO-JP02116.
XX
PR   18-JUL-1997;   97JP-0194445.
PR   15-MAY-1997;   97JP-0125505.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
PI   Ishii K,  Sato K,  Tunenari T;
XX
DR   WPI; 1999-070101/06.
XX
PT   Inhibitors of binding of parathyroid hormone related peptide to its
PT   receptor - useful for, e.g. treatment of cachexia arising from
PT   cancer or other diseases
XX
PS   Example 4; Page 66; 125pp; Japanese.
XX
CC   The present invention describes compositions for the treatment of
CC   cachexia containing a substance which inhibits the binding of a
CC   parathyroid hormone related peptide (PTHrP) to its receptor, as an
CC   active component. This substance may be an antagonist to the receptor,
CC   or an antibody (preferably monoclonal) or antibody fragment,
CC   recognising PTHrP. The antibody is preferably humanised or chimeric.
CC   The present invention also describes a humanised antibody prepared
CC   by hybridoma 23-57-137-1 (FERM BP-5631). The composition is used for
CC   the treatment of cachexia arising in connection with diseases such as
CC   cancer, thereby improving the quality of life of the patient. The
CC   present sequence represents a PCR primer used in an example from the
CC   present invention.
XX
SQ   Sequence 30 BP; 4 A; 7 C; 10 G; 9 T; 0 other;


  Query Match             100.0%;  Score 11;  DB 20;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ccccatggtgg 11
           ||||||||||||
Db      21 CCCCATGGTGG 11


RESULT  13
Z58895/c
ID   Z58895 standard; DNA; 30 BP.
XX
AC   Z58895;
XX
DT   26-APR-2000  (first entry)
XX
DE   PCR primer MBC1HVS1.
XX
KW   Hypercalcemic crisis; parathyroid hormone related peptide; PTHrP;
KW   human; tumour; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO200000219-A1.
XX
PD   06-JAN-2000.
XX
PF   25-JUN-1999;   99WO-JP03433.
XX
PR   26-JUN-1998;   98JP-0180143.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
PI   Sato K,  Tsunenari T;
XX
DR   WPI; 2000-117115/10.
XX
PT   Treatment of hypercalcemic crisis with a substance inhibiting binding
PT   of parathyroid hormone related peptide to its receptor -
XX
PS   Example 4; Page 80; 120pp; Japanese.
XX
CC   The invention relates to a method of treatment of hypercalcemic crisis.
CC   A composition for the treatment of hypercalcemic crisis contains as
CC   active component a substance which inhibits the binding of parathyroid
CC   hormone related peptide (PTHrP) to its receptor. The inhibitor is used
CC   for the treatment of hypercalcemic crisis, such as that associated with
CC   a malignant tumour.
XX
SQ   Sequence 30 BP; 4 A; 7 C; 10 G; 9 T; 0 other;


  Query Match             100.0%;  Score 11;  DB 21;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ccccatggtgg 11
           ||||||||||||
Db      21 CCCCATGGTGG 11


RESULT  14
T68725/c
ID   T68725 standard; DNA; 31 BP.
XX
AC   T68725;
XX
DT   01-SEP-1997  (first entry)
XX
DE   Human osteo antiviral protein 5' PCR primer.
XX
KW   Osteo antiviral protein; OAP; polymerase chain reaction; PCR;
KW   primer; ss.
XX
OS   Synthetic.
XX
PN   WO9722623-A1.
XX
PD   26-JUN-1997.
XX
PF   19-DEC-1995;   95WO-US17107.
XX
PR   19-DEC-1995;   95WO-US17107.
```

```
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Dillon PJ,  Feng P,  Gentz R,  Ni J;
XX
DR   WPI; 1997-341629/31.
XX
PT   DNA encoding osteo antiviral protein - useful as an antiviral agent,
PT   especially to treat necrotising pancreatitis caused by picornavirus
XX
PS   Example 2; Page 34; 63pp; English.
XX
CC   A 5' PCR primer (T68725) contains a BamHI restriction site followed
CC   by 18 nucleotides of the human osteo antiviral protein (OAP) coding
CC   sequence (see also T68722).  It was used with a 3' primer (T68726)
CC   for the PCR amplification of a DNA sequence (ATCC 97302) encoding
CC   full-length OAP.  The amplified DNA was incorporated into vector
CC   pcDNAI/Amp, and recombinant OAP (see also W19632) was expressed as
CC   an HA-tagged protein in transfected COS cells.
XX
SQ   Sequence 31 BP; 8 A; 11 C; 10 G; 2 T; 0 other;


  Query Match           100.0%;  Score 11;  DB 18;  Length 31;
  Best Local Similarity  100.0%;  Pred. No. 4.8e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ccccatggtgg 11
          ||||||||||| 
Db     19 CCCCATGGTGG 9


RESULT  15
V45332/c
ID   V45332 standard; DNA; 31 BP.
XX
AC   V45332;
XX
DT   27-OCT-1998  (first entry)
XX
DE   Human extracellular matrix-1 5'primer 2.
XX
KW   ss; human; extracellular matrix protein; hECM-1; osteogenesis; osteoma;
KW   angiogenesis; osteoblast; osteoclast; bone mineralisation; osteoporosis;
KW   revascularisation; osteodystrophy; osteohypertrophy; osteopetrusis;
KW   osteoblastoma; cancer; PCR; primer; amplification.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9831798-A1.
XX
PD   23-JUL-1998.
XX
PF   14-JAN-1998;   98WO-US00740.
XX
PR   18-JUN-1997;   97US-0050113.
PR   16-JAN-1997;   97US-0035711.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (UYAN-) UNIV ANTWERP.
XX
PI   Dillon PJ,  Feng P,  Gentz RL,  Merregaert J,  Ni J;
PI   Smits P;
XX
DR   WPI; 1998-414098/35.
XX
PT   New isolated human extracellular matrix-1 poly:peptide(s) - used to
PT   develop products for treating e.g. osteoporosis, wounds, ulcers,
PT   burns, arteriosclerosis, heart disease, osteodystrophy or cancer
XX
PS   Example 2; Page 27; 43pp; English.
XX
CC   The primers V45330-V45333 were used in the production of human
CC   extracellular matrix protein, hECM-1.  hECM-1 and splice variant
CC   hECM-1-SV1 can stimulate osteogenesis and angiogenesis (particularly in
CC   embryonic development).  They can be used to promote osteoblast and
CC   osteoclast differentiation and growth, as well as mineralisation of bone.
CC   In particular they can be used to promote bone growth, to treat
CC   osteoporosis, osteogenesis imperfecta and facilitate the healing of
CC   fractures.  They can also be used to promote angiogenesis, especially in
CC   early foetal development and, e.g. in revascularisation of transplanted
CC   or injured tissue.  Antagonists to the polypeptide can be used for
CC   treating osteodystrophy, osteohypertrophy, osteoma, osteopetrusis,
CC   osteoporosis, osteoblastoma, and cancer.
XX
SQ   Sequence 31 BP; 8 A; 11 C; 10 G; 2 T; 0 other;


  Query Match           100.0%;  Score 11;  DB 19;  Length 31;
  Best Local Similarity  100.0%;  Pred. No. 4.8e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ccccatggtgg 11
          ||||||||||| 
Db     19 CCCCATGGTGG 9


Search completed: March 23, 2001, 16:04:40
Job time: 35939 sec
```

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 23, 2001, 15:55:15 ; Search time 319.44 Seconds
(without alignments)
5.550 Million cell updates/sec

Title: US-09-554-267-18
Perfect score: 11
Sequence: 1 ccccatggtgg 11

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 280836 seqs, 80580151 residues

Total number of hits satisfying chosen parameters: 402106

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	11	100.0	15	5	5217867-3	Patent No. 5217867
c 2	11	100.0	21	2	US-08-876-991-8	Sequence 8, Appli
c 3	11	100.0	21	2	US-09-059-853-8	Sequence 8, Appli
c 4	11	100.0	24	2	US-08-785-750-11	Sequence 11, Appl
c 5	11	100.0	27	1	US-08-184-012C-9	Sequence 9, Appli
6	11	100.0	30	3	US-08-557-210A-25	Sequence 25, Appl
7	11	100.0	31	1	US-08-184-012C-10	Sequence 10, Appl
c 8	11	100.0	31	3	US-09-113-309-11	Sequence 11, Appl
c 9	11	100.0	34	3	US-09-067-089-5	Sequence 5, Appli
c 10	11	100.0	41	2	US-08-761-277A-56	Sequence 56, Appl
c 11	11	100.0	41	2	US-08-761-277A-67	Sequence 67, Appl
12	11	100.0	45	2	US-08-484-993B-51	Sequence 51, Appl
13	11	100.0	45	2	US-08-484-158B-51	Sequence 51, Appl
14	11	100.0	45	2	US-08-484-596A-51	Sequence 51, Appl
15	11	100.0	45	2	US-08-480-150A-51	Sequence 51, Appl
16	11	100.0	45	3	US-08-458-731-51	Sequence 51, Appl
17	11	100.0	45	3	US-08-149-223A-51	Sequence 51, Appl
c 18	11	100.0	47	1	US-08-334-177-5	Sequence 5, Appli
c 19	11	100.0	47	3	US-08-479-744A-48	Sequence 48, Appl
c 20	11	100.0	47	3	US-08-280-757B-48	Sequence 48, Appl
c 21	11	100.0	47	4	PCT-US95-13830-5	Sequence 5, Appli
c 22	10	90.9	20	2	US-08-943-208-3	Sequence 3, Appli
c 23	10	90.9	20	2	US-08-765-783A-70	Sequence 70, Appl
c 24	10	90.9	20	2	US-08-904-901-117	Sequence 117, App
c 25	10	90.9	20	3	US-08-921-100-70	Sequence 70, Appl
c 26	10	90.9	20	3	US-08-880-142-70	Sequence 70, Appl
c 27	10	90.9	20	3	US-08-902-201-70	Sequence 70, Appl
c 28	10	90.9	20	3	US-09-249-730-117	Sequence 117, App
c 29	10	90.9	23	3	US-08-974-549A-552	Sequence 552, App
c 30	10	90.9	24	1	US-08-443-640-23	Sequence 23, Appl
c 31	10	90.9	24	1	US-08-261-660A-7	Sequence 7, Appli
32	10	90.9	24	2	US-08-812-003-3	Sequence 3, Appli
c 33	10	90.9	24	4	PCT-US94-06931-7	Sequence 7, Appli
c 34	10	90.9	24	5	5223610-10	Patent No. 5223610
c 35	10	90.9	27	1	US-08-503-730-44	Sequence 44, Appl
c 36	10	90.9	27	2	US-08-816-605-7	Sequence 7, Appli
37	10	90.9	27	2	US-08-407-900B-2	Sequence 2, Appli
c 38	10	90.9	29	3	US-09-178-610-2	Sequence 2, Appli
c 39	10	90.9	30	3	US-09-192-048-11	Sequence 11, Appl
40	10	90.9	30	3	US-09-192-048-12	Sequence 12, Appl
c 41	10	90.9	32	1	US-08-137-117D-73	Sequence 73, Appl
c 42	10	90.9	32	1	US-08-436-717-73	Sequence 73, Appl
c 43	10	90.9	32	3	US-09-203-623-38	Sequence 38, Appl
c 44	10	90.9	33	1	US-08-086-439C-4	Sequence 4, Appli
c 45	10	90.9	33	1	US-08-434-877-4	Sequence 4, Appli

ALIGNMENTS

```
RESULT   1
5217867-3/c
;Patent No. 5217867
;     APPLICANT: EVANS, RONALD M.;HOLLENBERG, STANLEY M.
;     TITLE OF INVENTION: RECEPTORS THEIR IDENTIFICATION,
;CHARACTERIZATION, PREPARATION AND USE
;     NUMBER OF SEQUENCES: 4
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/278,614
;       FILING DATE: 30-NOV-1988
;SEQ ID NO:3:
;       LENGTH: 15
5217867-3


  Query Match             100.0%;  Score 11;  DB 5;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ccccatggtgg 11
             ||||||||||
Db      14 CCCCATGGTGG 4


RESULT   2
US-08-876-991-8/c
; Sequence 8, Application US/08876991
; Patent No. 5925360
;  GENERAL INFORMATION:
;     APPLICANT:  Gregor Meyers, Tillmann R menapf,
;     APPLICANT:  Heinz-J rgen Thiel
;     TITLE OF INVENTION:  Hog cholera virus vaccine and diagnostic
;     NUMBER OF SEQUENCES:  13
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Organon Teknika Corporation
;       ADDRESSEE:  Biotechnology Research Institute
;       STREET:  1330-A Piccard Drive
;       CITY:  Rockville
;       STATE:  Maryland
;       COUNTRY:  U.S.A.
;       ZIP:  20850
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/876,991
;       FILING DATE:  16-JUN-1997
;       CLASSIFICATION:  424
;     PRIOR APPLICATION DATA:
```

```
;      APPLICATION NUMBER:  US/08/747,577
;      FILING DATE:
;      APPLICATION NUMBER:  US/08/650,584
;      FILING DATE:
;      APPLICATION NUMBER:  US/08/469,702
;      FILING DATE:
;      APPLICATION NUMBER:  US/08/123,596
;      FILING DATE:
;      APPLICATION NUMBER:  07/797,554
;      FILING DATE:  22-NOV-1991
;      APPLICATION NUMBER:  US 07/494,991
;      FILING DATE:  16-MAR-1990
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  William M. Blackstone
;      REGISTRATION NUMBER:  29,772
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 258-5200
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  1..21
;      OTHER INFORMATION:  /label= Adaptor_4
;      OTHER INFORMATION:  /note= "Upper strand of Bgl II - BamH I adaptor"
US-08-876-991-8


  Query Match             100.0%;  Score 11;  DB 2;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ccccatggtgg 11
          ||||||||||
Db     14 CCCCATGGTGG 4


RESULT   3
US-09-059-853-8/c
; Sequence 8, Application US/09059853
; Patent No. 5935582
;  GENERAL INFORMATION:
;    APPLICANT:  Gregor Meyers, Tillmann R menapf,
;    APPLICANT:  Heinz-J rgen Thiel
;    TITLE OF INVENTION:  Hog cholera virus vaccine and diagnostic
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Organon Teknika Corporation
;      ADDRESSEE:  Biotechnology Research Institute
;      STREET:  1330-A Piccard Drive
;      CITY:  Rockville
;      STATE:  Maryland
;      COUNTRY:  U.S.A.
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/059,853
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/797,554
;      FILING DATE:  22-NOV-1991
;      APPLICATION NUMBER:  US 07/494,991
;      FILING DATE:  16-MAR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  William M. Blackstone
;      REGISTRATION NUMBER:  29,772
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 258-5200
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  1..21
;      OTHER INFORMATION:  /label= Adaptor_4
;      OTHER INFORMATION:  /note= "Upper strand of Bgl II - BamH I adaptor"
US-09-059-853-8


  Query Match             100.0%;  Score 11;  DB 2;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ccccatggtgg 11
          ||||||||||
Db     14 CCCCATGGTGG 4


RESULT   4
US-08-785-750-11/c
; Sequence 11, Application US/08785750
; Patent No. 5846528
;  GENERAL INFORMATION:
;    APPLICANT:  PODSAKOFF, GREGORY M.
;    APPLICANT:  KURTZMAN, GARY J.
;    TITLE OF INVENTION:  METHODS OF TREATING ANEMIA USING
;    TITLE OF INVENTION:  RECOMBINANT ADENO-ASSOCIATED VIRUS VIRIONS
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ROBINS & ASSOCIATES
;      STREET:  90 MIDDLEFIELD ROAD, SUITE 200
;      CITY:  MENLO PARK
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/785,750
;      FILING DATE:  16-JAN-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/588,355
;      FILING DATE:  18-JAN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MCCRACKEN, THOMAS P.
;      REGISTRATION NUMBER:  38,548
;      REFERENCE/DOCKET NUMBER:  0800-0009.21
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 325-7812
;      TELEFAX:  (415)325-7823
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-785-750-11
```

```
  Query Match           100.0%;  Score 11;  DB 2;  Length 24;
  Best Local Similarity  100.0%;  Pred. No. 3.9e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ccccatggtgg 11
          ||||||||||||
Db     20 CCCCATGGTGG 10


RESULT   5
US-08-184-012C-9/c
; Sequence 9, Application US/08184012C
; Patent No. 5606029
;  GENERAL INFORMATION:
;    APPLICANT:  Degen, Sandra J. F.
;    TITLE OF INVENTION:  Gene for a growth factor and its cDNA and
;    TITLE OF INVENTION:  protein
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Gregory Lunn
;      STREET:  Wood, Herron & Evans, 2700 Carew Tower
;      CITY:  Cincinnati
;      STATE:  Ohio
;      COUNTRY:  USA
;      ZIP:  45202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch,  800 Kb
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Macintosh 7.5.2
;      SOFTWARE:  Microsoft Word 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/184,012C
;      FILING DATE:  1/18/94
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lunn, Gregory
;      REGISTRATION NUMBER:  29,945
;      REFERENCE/DOCKET NUMBER:  CMC 57
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (513) 241-2324
;      TELEFAX:  (513) 421-7269
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;      DESCRIPTION:  This is an oligonucleotide used
;      DESCRIPTION:  with SEQ ID NO:10 to form a 5' end adaptor to
;      DESCRIPTION:  construct the cDNA in SEQ ID NO:7
;    ANTI-SENSE:  no
;    PUBLICATION INFORMATION:
;      RELEVANT RESIDUES IN SEQ ID NO:  1:  FROM 1 TO 27
US-08-184-012C-9


  Query Match           100.0%;  Score 11;  DB 1;  Length 27;
  Best Local Similarity  100.0%;  Pred. No. 3.9e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ccccatggtgg 11
          ||||||||||||
Db     18 CCCCATGGTGG 8


RESULT   6
US-08-557-210A-25
; Sequence 25, Application US/08557210A
; Patent No. 6114146
;  GENERAL INFORMATION:
;    APPLICANT:  Herlitschka, Sabine
;    APPLICANT:  Schlokat, Uwe
;    APPLICANT:  Falkner, Falko Guenther
;    APPLICANT:  Dorner, Friedrich
;    TITLE OF INVENTION:  An expression plasmid, a fusion protein, a
;    TITLE OF INVENTION:  transfected eukaryotic cell line, a method of producing for
;    TITLE OF INVENTION:  proteins, a foreign protein preparation as well as a pharma
;    TITLE OF INVENTION:  composition
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/557,210A
;      FILING DATE:  14-NOV-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  A 2099/94
;      FILING DATE:  14-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ISACSON, John P.
;      REGISTRATION NUMBER:  33,715
;      REFERENCE/DOCKET NUMBER:  040433/0142/SOPA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  30 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-557-210A-25


  Query Match           100.0%;  Score 11;  DB 3;  Length 30;
  Best Local Similarity  100.0%;  Pred. No. 3.9e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ccccatggtgg 11
          ||||||||||||
Db     10 CCCCATGGTGG 20


RESULT   7
US-08-184-012C-10
; Sequence 10, Application US/08184012C
; Patent No. 5606029
;  GENERAL INFORMATION:
;    APPLICANT:  Degen, Sandra J. F.
;    TITLE OF INVENTION:  Gene for a growth factor and its cDNA and
;    TITLE OF INVENTION:  protein
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Gregory Lunn
;      STREET:  Wood, Herron & Evans, 2700 Carew Tower
;      CITY:  Cincinnati
;      STATE:  Ohio
;      COUNTRY:  USA
;      ZIP:  45202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch,  800 Kb
```

```
;       COMPUTER:  Apple Macintosh
;       OPERATING SYSTEM:  Macintosh 7.5.2
;       SOFTWARE:  Microsoft Word 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/184,012C
;       FILING DATE:  1/18/94
;       CLASSIFICATION:  536
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Lunn, Gregory
;       REGISTRATION NUMBER:  29,945
;       REFERENCE/DOCKET NUMBER:  CMC 57
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (513) 241-2324
;       TELEFAX:  (513) 421-7269
;   INFORMATION FOR SEQ ID NO:  10:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  31 bases
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA to mRNA
;       DESCRIPTION:  This is an oligonucleotide used
;       DESCRIPTION:  with SEQ ID NO:9 to form a 5' end adaptor to
;       DESCRIPTION:  construct the cDNA in SEQ ID NO:7
;     ANTI-SENSE:  yes
;     PUBLICATION INFORMATION:
;       RELEVANT RESIDUES IN SEQ ID NO:  1:  FROM 1 TO 31
US-08-184-012C-10


  Query Match             100.0%;  Score 11;  DB 1;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ccccatggtgg 11
          ||||||||||| 
Db     14 CCCCATGGTGG 24


RESULT   8
US-09-113-309-11/c
; Sequence 11, Application US/09113309A
; Patent No. 6110738
; GENERAL INFORMATION:
;  APPLICANT: Zhou, Shibin
;  APPLICANT: Zawel, Leigh
;  APPLICANT: Vogelstein, Bert
;  APPLICANT: Kinzler, Kenneth
;  TITLE OF INVENTION: Human Fast-1 Gene
;  FILE REFERENCE: 01107.10898
;  CURRENT APPLICATION NUMBER: US/09/113,309A
;  CURRENT FILING DATE: 1998-07-10
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
;   LENGTH: 31
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-113-309-11


  Query Match             100.0%;  Score 11;  DB 3;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ccccatggtgg 11
          ||||||||||| 
Db     21 CCCCATGGTGG 11


RESULT   9
US-09-067-089-5/c
; Sequence 5, Application US/09067089A
; Patent No. 6140093
; GENERAL INFORMATION:
;  APPLICANT: Hudson, Peter L.
;  APPLICANT: He, Wei W.
;  APPLICANT: Ruben, Steven M.
;  TITLE OF INVENTION: Serum Paraoxnase
;  FILE REFERENCE: PF124D2
;  CURRENT APPLICATION NUMBER: US/09/067,089A
;  CURRENT FILING DATE: 1998-04-27
;  EARLIER APPLICATION NUMBER: 08/783,889
;  EARLIER FILING DATE: 1997-01-16
;  EARLIER APPLICATION NUMBER: 08/270,583
;  EARLIER FILING DATE: 1994-07-05
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 34
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-067-089-5


  Query Match             100.0%;  Score 11;  DB 3;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ccccatggtgg 11
          ||||||||||| 
Db     19 CCCCATGGTGG 9


RESULT  10
US-08-761-277A-56/c
; Sequence 56, Application US/08761277A
; Patent No. 5972334
;  GENERAL INFORMATION:
;    APPLICANT:  Denney Jr., Dan W.
;    TITLE OF INVENTION:  Vaccines For Treatment Of Lymphoma And
;    TITLE OF INVENTION:  Leukemia
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/761,277A
;      FILING DATE:  06-DEC-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/644,664
;      FILING DATE:  01-MAY-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MacKnight, Kamrin T.
;      REGISTRATION NUMBER:  38,230
;      REFERENCE/DOCKET NUMBER:  GENITOPE-02406
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  56:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  41 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
```

US-08-761-277A-56

Query Match 100.0%; Score 11; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 ccccatggtgg 11
           ||||||||||| 
Db      27 CCCCATGGTGG 17
```

```
RESULT  11
US-08-761-277A-67/c
; Sequence 67, Application US/08761277A
; Patent No. 5972334
;  GENERAL INFORMATION:
;    APPLICANT:  Denney Jr., Dan W.
;    TITLE OF INVENTION:  Vaccines For Treatment Of Lymphoma And
;    TITLE OF INVENTION:  Leukemia
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/761,277A
;      FILING DATE:  06-DEC-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/644,664
;      FILING DATE:  01-MAY-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MacKnight, Kamrin T.
;      REGISTRATION NUMBER:  38,230
;      REFERENCE/DOCKET NUMBER:  GENITOPE-02406
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  67:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  41 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-761-277A-67
```

Query Match 100.0%; Score 11; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 ccccatggtgg 11
           ||||||||||| 
Db      27 CCCCATGGTGG 17
```

```
RESULT  12
US-08-484-993B-51
; Sequence 51, Application US/08484993B
; Patent No. 5837497
;  GENERAL INFORMATION:
;    APPLICANT:  Harris Ph.D., Jeffrey D.
;    APPLICANT:  Hsu, Kuang T.
;    APPLICANT:  Podolski, Joseph S.
;    TITLE OF INVENTION:  Materials and Methods for Immunocontraception
;    NUMBER OF SEQUENCES:  59
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/484,993B
;      FILING DATE:  09-NOV-1993
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/012,990
;      FILING DATE:  29-JAN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/973,341
;      FILING DATE:  09-NOV-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clough, David W.
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  31745
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6653
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  51:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  45 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-484-993B-51
```

Query Match 100.0%; Score 11; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 ccccatggtgg 11
           ||||||||||| 
Db       4 CCCCATGGTGG 14
```

```
RESULT  13
US-08-484-158B-51
; Sequence 51, Application US/08484158B
; Patent No. 5976545
;  GENERAL INFORMATION:
;    APPLICANT:  Harris Ph.D., Jeffrey D.
;    APPLICANT:  Hsu, Kuang T.
;    APPLICANT:  Podolski, Joseph S.
;    TITLE OF INVENTION:  Pharmaceutical Compositions for
;    TITLE OF INVENTION:  Immunocontraception
;    NUMBER OF SEQUENCES:  61
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
```

```
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/484,158B
;       FILING DATE:  07-JUNE-95
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/149,223
;       FILING DATE:  09-NOV-93
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/012,990
;       FILING DATE:  29-JAN-93
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/973,341
;       FILING DATE:  09-NOV-92
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Clough, David W.
;       REGISTRATION NUMBER:  36,107
;       REFERENCE/DOCKET NUMBER:  32794
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  312/474-6653
;       TELEFAX:  312/474-0448
;       TELEX:  25-3856
;   INFORMATION FOR SEQ ID NO:  51:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  45 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA
US-08-484-158B-51


  Query Match             100.0%;  Score 11;  DB 2;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ccccatggtgg 11
           ||||||||||| 
Db       4 CCCCATGGTGG 14


RESULT  14
US-08-484-596A-51
; Sequence 51, Application US/08484596A
; Patent No. 5981228
;  GENERAL INFORMATION:
;    APPLICANT:  Harris Ph.D., Jeffrey D.
;    APPLICANT:  Hsu, Kuang T.
;    APPLICANT:  Podolski, Joseph S.
;    TITLE OF INVENTION:  Materials and Methods for Immunocontraception
;    NUMBER OF SEQUENCES:  59
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/484,596A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/149,223
;      FILING DATE:  11-NOV-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/973,341
;      FILING DATE:  09-NOV-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clough, David W.
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  31745
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6653
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  51:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  45 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-484-596A-51


  Query Match             100.0%;  Score 11;  DB 2;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ccccatggtgg 11
           ||||||||||| 
Db       4 CCCCATGGTGG 14


RESULT  15
US-08-480-150A-51
; Sequence 51, Application US/08480150A
; Patent No. 5989550
;  GENERAL INFORMATION:
;    APPLICANT:  Harris Ph.D., Jeffrey D.
;    APPLICANT:  Hsu, Kuang T.
;    APPLICANT:  Podolski, Joseph S.
;    TITLE OF INVENTION:  Materials and Methods for Immunocontraception
;    NUMBER OF SEQUENCES:  59
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/480,150A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/149,223
;      FILING DATE:  09-NOV-1993
;      APPLICATION NUMBER:  08/012,990
;      FILING DATE:  29-JAN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/973,341
;      FILING DATE:  09-NOV-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clough, David W.
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  31745
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6653
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  51:
;    SEQUENCE CHARACTERISTICS:
```

; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-480-150A-51

Query Match 100.0%; Score 11; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 ccccatggtgg 11
           ||||||||||||
Db       4 CCCCATGGTGG 14
```

Search completed: March 23, 2001, 15:55:16
Job time: 35675 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 23, 2001, 16:04:40 ; Search time 551.33 Seconds
(without alignments)
7.495 Million cell updates/sec

Title: US-09-554-267-19
Perfect score: 11
Sequence: 1 agtcatggccc 11

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 624296

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_36:*
1: /cgn2_2/gcgdata/geneseq/geneseqn/NA1980.DAT:*
2: /cgn2_2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
3: /cgn2_2/gcgdata/geneseq/geneseqn/NA1982.DAT:*
4: /cgn2_2/gcgdata/geneseq/geneseqn/NA1983.DAT:*
5: /cgn2_2/gcgdata/geneseq/geneseqn/NA1984.DAT:*
6: /cgn2_2/gcgdata/geneseq/geneseqn/NA1985.DAT:*
7: /cgn2_2/gcgdata/geneseq/geneseqn/NA1986.DAT:*
8: /cgn2_2/gcgdata/geneseq/geneseqn/NA1987.DAT:*
9: /cgn2_2/gcgdata/geneseq/geneseqn/NA1988.DAT:*
10: /cgn2_2/gcgdata/geneseq/geneseqn/NA1989.DAT:*
11: /cgn2_2/gcgdata/geneseq/geneseqn/NA1990.DAT:*
12: /cgn2_2/gcgdata/geneseq/geneseqn/NA1991.DAT:*
13: /cgn2_2/gcgdata/geneseq/geneseqn/NA1992.DAT:*
14: /cgn2_2/gcgdata/geneseq/geneseqn/NA1993.DAT:*
15: /cgn2_2/gcgdata/geneseq/geneseqn/NA1994.DAT:*
16: /cgn2_2/gcgdata/geneseq/geneseqn/NA1995.DAT:*
17: /cgn2_2/gcgdata/geneseq/geneseqn/NA1996.DAT:*
18: /cgn2_2/gcgdata/geneseq/geneseqn/NA1997.DAT:*
19: /cgn2_2/gcgdata/geneseq/geneseqn/NA1998.DAT:*
20: /cgn2_2/gcgdata/geneseq/geneseqn/NA1999.DAT:*
21: /cgn2_2/gcgdata/geneseq/geneseqn/NA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	11	100.0	18	15	Q77640	Ribonucleotide to
	2	11	100.0	18	15	Q76399	Polynucleotide to
c	3	11	100.0	18	15	Q77654	Antisense ribonucl
c	4	11	100.0	18	15	Q77626	Antisense polynucl
c	5	11	100.0	20	18	T73615	Neuropeptide Y rec
c	6	11	100.0	20	20	Z08883	Human PECAM-1 anti
c	7	11	100.0	20	20	X83199	Human neuropeptide
	8	11	100.0	21	15	Q77642	Ribonucleotide to
	9	11	100.0	21	15	Q77644	Ribonucleotide to
	10	11	100.0	21	15	Q77614	Polynucleotide to
	11	11	100.0	21	15	Q77616	Polynucleotide to
c	12	11	100.0	21	15	Q77656	Antisense ribonucl
c	13	11	100.0	21	15	Q77658	Antisense ribonucl
c	14	11	100.0	21	15	Q77628	Antisense polynucl
c	15	11	100.0	21	15	Q77630	Antisense polynucl
	16	11	100.0	24	15	Q77641	Ribonuclectide to
	17	11	100.0	24	15	Q77643	Ribonuclectide to
	18	11	100.0	24	15	Q76400	Polynuclectide to
	19	11	100.0	24	15	Q77615	Polynucleotide to
	20	11	100.0	24	15	Q77617	Polynucleotide to
c	21	11	100.0	24	15	Q77655	Antisense ribonucl
c	22	11	100.0	24	15	Q77657	Antisense ribonucl
c	23	11	100.0	24	15	Q77659	Antisense ribonucl
c	24	11	100.0	24	15	Q77627	Antisense polynucl
c	25	11	100.0	24	15	Q77629	Antisense polynucl
c	26	11	100.0	24	15	Q77631	Antisense polynucl
	27	11	100.0	24	15	Q77645	Ribonucleotide to
	28	11	100.0	27	15	Q77618	Polynucleotide to
c	29	11	100.0	27	15	Q77660	Antisense ribonucl
	30	11	100.0	27	15	Q77646	Ribonucleotide to
c	31	11	100.0	27	15	Q77632	Antisense polynucl
c	32	10.2	92.7	18	15	Q76389	Polynucleotide to
	33	10.2	92.7	18	15	Q76388	Antisense polynucl
	34	10.2	92.7	18	15	Q76390	Antisense ribonucl
c	35	10.2	92.7	36	15	Q76387	Tenascin gene cons
	36	10.2	92.7	36	15	Q76386	Tenascin gene cons
c	37	10.2	92.7	36	15	Q77661	Tenascin gene mRNA
	38	10.2	92.7	36	15	Q77662	Tenascin gene mRNA
c	39	10	90.9	17	17	T39832	Primer D2 for HSP-
c	40	10	90.9	18	16	T51454	Rse.gD PCR primer
c	41	10	90.9	18	16	Q94147	Primer R1 for prod
	42	10	90.9	20	20	X92223	PCR primer used to
	43	10	90.9	21	20	Z34128	Human PRO944 PCR f
c	44	10	90.9	24	12	Q15082	T-cell receptor pr
c	45	10	90.9	24	16	Q91950	T-cell Receptor be

ALIGNMENTS

RESULT 1
Q77640
ID Q77640 standard; RNA; 18 BP.
XX
AC Q77640;
XX
DT 02-JUN-1995 (first entry)
XX
DE Ribonucleotide to tenascin gene consensus mRNA initiation site +1-+18.
XX
KW Antisense; polynucleotide; sense strand; tenascin; complementary;
KW consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW proliferation; growth stimulatory; transcription; vascular stenosis;
KW post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW organ transplant; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_difference 1..18
FT /*tag= a
FT /note= "phosphodiester bonds between nucleotides
FT may be replaced by phosphorothioate bonds"
XX
PN WO9421664-A.
XX
PD 29-SEP-1994.
XX
PF 24-MAR-1994; 94WO-US03206.
XX
PR 25-MAR-1993; 93US-0037025.
XX
PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI Denner LA, Dixon RAF, Rege AA, Stacy DL;

```
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 5; Page 49; 64pp; English.
XX
CC   A series of polynucleotides, either DNA (Q76388 and Q76392-400 and
CC   Q77614-18) or RNA (Q76390 and Q77633-46), directed against the consensus
CC   mRNA initiation site sequence (Q77661) for the tenascin gene.  The
CC   polynucleotides are based on the degenerate sequence (Q76386) of the
CC   tenascin gene.  Tenascin is an extracellular matrix glycoprotein
CC   consisting six disulphide-linked subunits, each having molecular mass of
CC   190-250 kDa.  Tenascin may be important for smooth muscle cell
CC   proliferation as the protein has growth stimulatory activity.  The
CC   polynucleotides can be used to inhibit transcription of the gene or
CC   translation of the mRNA encoding tenascin. The method is applicable to a
CC   number of diseases where the proliferation of smooth muscle is involved
CC   e.g. vascular stenosis, post-angioplasty restenosis and other
CC   non-angioplasty procedures such as cardiac hypertrophy, vascular surgery
CC   and organ transplant.
XX
SQ   Sequence 18 BP; 3 A; 7 C; 4 G; 4 U; 0 other;


  Query Match             100.0%;  Score 11;  DB 15;  Length 18;
  Best Local Similarity   81.8%;  Pred. No. 3e+02;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 agtcatggccc 11
          ||:||:|||||
Db      4 agucauggccc 14


RESULT   2
Q76399
ID   Q76399 standard; DNA; 18 BP.
XX
AC   Q76399;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Polynucleotide to tenascin gene consensus mRNA initiation site +1-+18.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..18
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                          may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 5; Page 42; 64pp; English.
XX
CC   A series of polynucleotides, either DNA (Q76388 and Q76392-400 and
CC   Q77614-18) or RNA (Q76390 and Q77633-46), directed against the consensus
CC   mRNA initiation site sequence (Q77661) for the tenascin gene.  The
CC   polynucleotides are based on the degenerate sequence (Q76386) of the
CC   tenascin gene.  Tenascin is an extracellular matrix glycoprotein
CC   consisting six disulphide-linked subunits, each having molecular mass of
CC   190-250 kDa.  Tenascin may be important for smooth muscle cell
CC   proliferation as the protein has growth stimulatory activity.  The
CC   polynucleotides can be used to inhibit transcription of the gene or
CC   translation of the mRNA encoding tenascin. The method is applicable to a
CC   number of diseases where the proliferation of smooth muscle is involved
CC   e.g. vascular stenosis, post-angioplasty restenosis and other
CC   non-angioplasty procedures such as cardiac hypertrophy, vascular surgery
CC   and organ transplant.
XX
SQ   Sequence 18 BP; 3 A; 7 C; 4 G; 4 T; 0 other;


  Query Match             100.0%;  Score 11;  DB 15;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 3e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 agtcatggccc 11
          ||||||||||||
Db      4 agtcatggccc 14


RESULT   3
Q77654/c
ID   Q77654 standard; RNA; 18 BP.
XX
AC   Q77654;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Antisense ribonucleotide binds to tenascin gene consensus at +1-+18.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..18
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                          may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
```

PT gene, useful for inhibiting vascular smooth muscle cell
PT proliferation.
XX
PS Claim 10; Page 52; 64pp; English.
XX
CC A series of antisense polynucleotides, either DNA (Q76388 and Q77619-32)
CC or RNA (Q76390 and Q77647-60) directed against the sense strand of the
CC gene encoding tenascin. The polynucleotides are based on the
CC complementary sequence (Q76386) of the consensus mRNA initiation site
CC sequence (Q77661) for the tenascin gene. Tenascin is an extracellular
CC matrix glycoprotein consisting six disulphide-linked subunits, each
CC having molecular mass of 190-250 kDa. Tenascin may be important for
CC smooth muscle cell proliferation as the protein has growth stimulatory
CC activity. The polynucleotides can be used to inhibit transcription
CC of the gene or translation of the mRNA encoding tenascin. The method is
CC applicable to a number of diseases where the proliferation of smooth
CC muscle is involved e.g. vascular stenosis, post-angioplasty restenosis
CC and other non-angioplasty procedures such as cardiac hypertrophy,
CC vascular surgery and organ transplant.
XX
SQ Sequence 18 BP; 3 A; 4 C; 7 G; 4 U; 0 other;

Query Match 100.0%; Score 11; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agtcatggccc 11
||||||||||||
Db 15 AGTCATGGCCC 5

RESULT 4
Q77626/c
ID Q77626 standard; DNA; 18 BP.
XX
AC Q77626;
XX
DT 02-JUN-1995 (first entry)
XX
DE Antisense polynucleotide binds to tenascin gene consensus at +1-+18.
XX
KW Antisense; polynucleotide; sense strand; tenascin; complementary;
KW consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW proliferation; growth stimulatory; transcription; vascular stenosis;
KW post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW organ transplant; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_difference 1..18
FT /*tag= a
FT /note= "phosphodiester bonds between nucleotides
FT may be replaced by phosphorothioate bonds"
XX
PN WO9421664-A.
XX
PD 29-SEP-1994.
XX
PF 24-MAR-1994; 94WO-US03206.
XX
PR 25-MAR-1993; 93US-0037025.
XX
PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI Denner LA, Dixon RAF, Rege AA, Stacy DL;
XX
DR WPI; 1994-316926/39.
XX
PT Synthetic anti-sense polynucleotide - hybridises to tenascin
PT gene, useful for inhibiting vascular smooth muscle cell
PT proliferation.
XX
PS Claim 10; Page 45; 64pp; English.
XX
CC A series of antisense polynucleotides, either DNA (Q76388 and Q77619-32)
CC or RNA (Q76390 and Q77647-60) directed against the sense strand of the
CC gene encoding tenascin. The polynucleotides are based on the
CC complementary sequence (Q76386) of the consensus mRNA initiation site
CC sequence (Q77661) for the tenascin gene. Tenascin is an extracellular
CC matrix glycoprotein consisting six disulphide-linked subunits, each
CC having molecular mass of 190-250 kDa. Tenascin may be important for
CC smooth muscle cell proliferation as the protein has growth stimulatory
CC activity. The polynucleotides can be used to inhibit transcription
CC of the gene or translation of the mRNA encoding tenascin. The method is
CC applicable to a number of diseases where the proliferation of smooth
CC muscle is involved e.g. vascular stenosis, post-angioplasty restenosis
CC and other non-angioplasty procedures such as cardiac hypertrophy,
CC vascular surgery and organ transplant.
XX
SQ Sequence 18 BP; 4 A; 4 C; 7 G; 3 T; 0 other;

Query Match 100.0%; Score 11; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agtcatggccc 11
||||||||||||
Db 15 AGTCATGGCCC 5

RESULT 5
T73615/c
ID T73615 standard; cDNA; 20 BP.
XX
AC T73615;
XX
DT 14-APR-1998 (first entry)
XX
DE Neuropeptide Y receptor (NPY Y5) PCR primer (reverse).
XX
KW Neuropeptide Y receptor Y5; NPY Y5; peptide YY; NPY/YY receptor;
KW rat; neurotransmitter; antagonist; agonist; obesity; anorexia;
KW hyperlipidaemia; diabetes; gene therapy; PCR; primer; ss.
XX
OS Synthetic.
OS Rattus sp.
XX
PN WO9737998-A2.
XX
PD 16-OCT-1997.
XX
PF 08-APR-1997; 97WO-US05781.
XX
PR 08-APR-1996; 96US-0014969.
XX
PA (FARB) BAYER CORP.
XX
PI Bloomquist BT, Cornfield LJ, Flores-Riveros JR, Hu Y;
PI McCaleb ML;
XX
DR WPI; 1997-512637/47.
XX
PT Nucleic acid molecule encoding neuropeptide Y receptor - useful to
PT identify antagonists and agonists, e.g. treat obesity, diabetes,
PT hyperlipidaemia and anorexia
XX
PS Example 5; Page 25; 49pp; English.
XX
CC This reverse PCR primer corresponds to nucleotides 843-862 of a
CC rat cDNA clone (see T87940) coding for novel neuropeptide Y
CC receptor NPY Y5. Is was used with a forward primer (see T73603)
CC to amplify a 375 bp coding region of rat NPY Y5 cDNA. This was
CC used to probe a human genomic DNA library. A DNA clone (see

```
CC   T73602) coding for human NPY Y5 (see W27604) wa isolated. Methods
CC   are provided for using the receptor to screen for antagonists and
CC   agonists useful for the treatment of obesity and anorexia,
CC   respectively.
XX
SQ   Sequence 20 BP; 6 A; 6 C; 5 G; 3 T; 0 other;


  Query Match             100.0%;  Score 11;  DB 18;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 agtcatggccc 11
          ||||||||||| 
Db     16 AGTCATGGCCC 6


RESULT   6
Z08883/c
ID   Z08883 standard; DNA; 20 BP.
XX
AC   Z08883;
XX
DT   15-NOV-1999  (first entry)
XX
DE   Human PECAM-1 antisense oligonucleotide SEQ ID NO:4.
XX
KW   Human; platelet endothelial cell adhesion molecule 1; PECAM-1;
KW   diagnosis; antisense oligonucleotide; CD31 antigen; endoCAM;
KW   phosphorothioate; autoimmune disorder; multiple sclerosis; cancer;
KW   Grave's disease; inflammatory disorder; allograft rejection; arthritis;
KW   Crohn's disease; dermatological condition; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1..20
FT                    /*tag= a
FT                    /note= "phosphorothioate linkages"
XX
PN   US5955443-A.
XX
PD   21-SEP-1999.
XX
PF   19-MAR-1998;   98US-0044506.
XX
PR   19-MAR-1998;   98US-0044506.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Bennett CF,  Zhang H,  Condon TP,  Flournoy SC;
XX
DR   WPI; 1999-539588/45.
XX
PT   Antisense oligonucleotides useful for diagnosing/treating autoimmune
PT   and inflammatory disorders and cancer  -
XX
PS   Claim 1; Column 36; 56pp; English.
XX
CC   The present sequence represents a human platelet endothelial cell
CC   adhesion molecule 1 (PECAM-1) antisense oligonucleotide (OGN), which
CC   hybridises with a region of the nucleic acid encoding a human PECAM-1
CC   and decreases its expression. PECAM-1 antisense OGNs may be used for
CC   the diagnosis and treatment of autoimmune disorders (multiple sclerosis
CC   or Grave's disease), inflammatory disorders (arthritis, allograft
CC   rejections and Crohn's disease), dermatological conditions, and cancer.
CC   Antisense OGNs from the present invention are more effective at
CC   blocking the action of PECAM-1 compared to monoclonal antibodies and
CC   synthetic peptides since they are smaller and therefore have better
CC   access to sites of inflammation.
XX
SQ   Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 other;


  Query Match             100.0%;  Score 11;  DB 20;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 agtcatggccc 11
          ||||||||||| 
Db     13 AGTCATGGCCC 3


RESULT   7
X83199/c
ID   X83199 standard; DNA; 20 BP.
XX
AC   X83199;
XX
DT   31-AUG-1999  (first entry)
XX
DE   Human neuropeptide Y5 receptor coding sequence - primer.
XX
KW   Human; neuropeptide Y; NPY; receptor; hypothalamus; antagonist; agonist;
KW   obesity; diabetes; antibody; detection; primer; PCR; amplification; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US5919901-A.
XX
PD   06-JUL-1999.
XX
PF   08-APR-1996;   96US-0630118.
XX
PR   08-APR-1996;   96US-0630118.
XX
PA   (FARB ) BAYER CORP.
XX
PI   Bloomquist BT,  Cornfield LJ,  Flores-Riveros JR,  Hu Y;
PI   McCaleb ML;
XX
DR   WPI; 1999-394648/33.
XX
PT   Neuropeptide Y receptor Y5 and related nucleic acid
XX
PS   Example 5; Column 16; 23pp; English.
XX
CC   Primers X83198-X83199 were used to PCR amplify the human neuropeptide
CC   Y5 receptor (Y5) coding sequence (X83197).  The protein is useful for
CC   screening for compounds able to be used as agonists and antagonists to
CC   the Y5 receptor, especially for the treatment obesity and diabetes and
CC   for developing antibodies for the detection of the protein.
XX
SQ   Sequence 20 BP; 6 A; 6 C; 5 G; 3 T; 0 other;


  Query Match             100.0%;  Score 11;  DB 20;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 agtcatggccc 11
          ||||||||||| 
Db     16 AGTCATGGCCC 6


RESULT   8
Q77642
ID   Q77642 standard; RNA; 21 BP.
XX
AC   Q77642;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Ribonucleotide to tenascin gene consensus mRNA initiation site -3-+18.
```

```
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..21
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                          may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 5; Page 49; 64pp; English.
XX
CC   A series of polynucleotides, either DNA (Q76388 and Q76392-400 and
CC   Q77614-18) or RNA (Q76390 and Q77633-46), directed against the consensus
CC   mRNA initiation site sequence (Q77661) for the tenascin gene.  The
CC   polynucleotides are based on the degenerate sequence (Q76386) of the
CC   tenascin gene.  Tenascin is an extracellular matrix glycoprotein
CC   consisting six disulphide-linked subunits, each having molecular mass of
CC   190-250 kDa.  Tenascin may be important for smooth muscle cell
CC   proliferation as the protein has growth stimulatory activity.  The
CC   polynucleotides can be used to inhibit transcription of the gene or
CC   translation of the mRNA encoding tenascin. The method is applicable to a
CC   number of diseases where the proliferation of smooth muscle is involved
CC   e.g. vascular stenosis, post-angioplasty restenosis and other
CC   non-angioplasty procedures such as cardiac hypertrophy, vascular surgery
CC   and organ transplant.
XX
SQ   Sequence 21 BP; 3 A; 7 C; 6 G; 5 U; 0 other;


  Query Match             100.0%;  Score 11;  DB 15;  Length 21;
  Best Local Similarity   81.8%;  Pred. No. 3e+02;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 agtcatggccc 11
           ||:||:|||||
Db       4 agucauggccc 14


RESULT   9
Q77644
ID   Q77644 standard; RNA; 21 BP.
XX
AC   Q77644;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Ribonucleotide to tenascin gene consensus mRNA initiation site +1-+21.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..21
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                          may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 5; Page 50; 64pp; English.
XX
CC   A series of polynucleotides, either DNA (Q76388 and Q76392-400 and
CC   Q77614-18) or RNA (Q76390 and Q77633-46), directed against the consensus
CC   mRNA initiation site sequence (Q77661) for the tenascin gene.  The
CC   polynucleotides are based on the degenerate sequence (Q76386) of the
CC   tenascin gene.  Tenascin is an extracellular matrix glycoprotein
CC   consisting six disulphide-linked subunits, each having molecular mass of
CC   190-250 kDa.  Tenascin may be important for smooth muscle cell
CC   proliferation as the protein has growth stimulatory activity.  The
CC   polynucleotides can be used to inhibit transcription of the gene or
CC   translation of the mRNA encoding tenascin. The method is applicable to a
CC   number of diseases where the proliferation of smooth muscle is involved
CC   e.g. vascular stenosis, post-angioplasty restenosis and other
CC   non-angioplasty procedures such as cardiac hypertrophy, vascular surgery
CC   and organ transplant.
XX
SQ   Sequence 21 BP; 4 A; 8 C; 5 G; 4 U; 0 other;


  Query Match             100.0%;  Score 11;  DB 15;  Length 21;
  Best Local Similarity   81.8%;  Pred. No. 3e+02;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 agtcatggccc 11
           ||:||:|||||
Db       7 agucauggccc 17


RESULT  10
Q77614
ID   Q77614 standard; DNA; 21 BP.
XX
AC   Q77614;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Polynucleotide to tenascin gene consensus mRNA initiation site -3-+18.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
```

```
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..21
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                          may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 5; Page 42; 64pp; English.
XX
CC   A series of polynucleotides, either DNA (Q76388 and Q76392-400 and
CC   Q77614-18) or RNA (Q76390 and Q77633-46), directed against the consensus
CC   mRNA initiation site sequence (Q77661) for the tenascin gene.  The
CC   polynucleotides are based on the degenerate sequence (Q76386) of the
CC   tenascin gene.  Tenascin is an extracellular matrix glycoprotein
CC   consisting six disulphide-linked subunits, each having molecular mass of
CC   190-250 kDa.  Tenascin may be important for smooth muscle cell
CC   proliferation as the protein has growth stimulatory activity.  The
CC   polynucleotides can be used to inhibit transcription of the gene or
CC   translation of the mRNA encoding tenascin. The method is applicable to a
CC   number of diseases where the proliferation of smooth muscle is involved
CC   e.g. vascular stenosis, post-angioplasty restenosis and other
CC   non-angioplasty procedures such as cardiac hypertrophy, vascular surgery
CC   and organ transplant.
XX
SQ   Sequence 21 BP; 3 A; 7 C; 6 G; 5 T; 0 other;


  Query Match           100.0%;  Score 11;  DB 15;  Length 21;
  Best Local Similarity  100.0%;  Pred. No. 3e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 agtcatggccc 11
          ||||||||||| |
Db      4 agtcatggccc 14


RESULT  11
Q77616
ID   Q77616 standard; DNA; 21 BP.
XX
AC   Q77616;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Polynucleotide to tenascin gene consensus mRNA initiation site +1-+21.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..21
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                          may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 5; Page 43; 64pp; English.
XX
CC   A series of polynucleotides, either DNA (Q76388 and Q76392-400 and
CC   Q77614-18) or RNA (Q76390 and Q77633-46), directed against the consensus
CC   mRNA initiation site sequence (Q77661) for the tenascin gene.  The
CC   polynucleotides are based on the degenerate sequence (Q76386) of the
CC   tenascin gene.  Tenascin is an extracellular matrix glycoprotein
CC   consisting six disulphide-linked subunits, each having molecular mass of
CC   190-250 kDa.  Tenascin may be important for smooth muscle cell
CC   proliferation as the protein has growth stimulatory activity.  The
CC   polynucleotides can be used to inhibit transcription of the gene cr
CC   translation of the mRNA encoding tenascin. The method is applicable to a
CC   number of diseases where the proliferation of smooth muscle is involved
CC   e.g. vascular stenosis, post-angioplasty restenosis and other
CC   non-angioplasty procedures such as cardiac hypertrophy, vascular surgery
CC   and organ transplant.
XX
SQ   Sequence 21 BP; 4 A; 8 C; 5 G; 4 T; 0 other;


  Query Match           100.0%;  Score 11;  DB 15;  Length 21;
  Best Local Similarity  100.0%;  Pred. No. 3e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 agtcatggccc 11
          ||||||||||| |
Db      7 agtcatggccc 17


RESULT  12
Q77656/c
ID   Q77656 standard; RNA; 21 BP.
XX
AC   Q77656;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Antisense ribonucleotide binds to tenascin gene consensus at -3-+18.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
```

```
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..21
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                          may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 10; Page 53; 64pp; English.
XX
CC   A series of antisense polynucleotides, either DNA (Q76388 and Q77619-32)
CC   or RNA (Q76390 and Q77647-60) directed against the sense strand of the
CC   gene encoding tenascin.  The polynucleotides are based on the
CC   complementary sequence (Q76386) of the consensus mRNA initiation site
CC   sequence (Q77661) for the tenascin gene.  Tenascin is an extracellular
CC   matrix glycoprotein consisting six disulphide-linked subunits, each
CC   having molecular mass of 190-250 kDa.  Tenascin may be important for
CC   smooth muscle cell proliferation as the protein has growth stimulatory
CC   activity.  The polynucleotides can be used to inhibit transcription
CC   of the gene or translation of the mRNA encoding tenascin.  The method is
CC   applicable to a number of diseases where the proliferation of smooth
CC   muscle is involved e.g. vascular stenosis, post-angioplasty restenosis
CC   and other non-angioplasty procedures such as cardiac hypertrophy,
CC   vascular surgery and organ transplant.
XX
SQ   Sequence 21 BP; 5 A; 6 C; 7 G; 3 U; 0 other;

  Query Match             100.0%;  Score 11;  DB 15;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 agtcatggccc 11
           ||||||||||| |
Db      18 AGTCATGGCCC 8


RESULT  13
Q77658/c
ID   Q77658 standard; RNA; 21 BP.
XX
AC   Q77658;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Antisense ribonucleotide binds to tenascin gene consensus at +1-+21.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..21
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                          may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 10; Page 53; 64pp; English.
XX
CC   A series of antisense polynucleotides, either DNA (Q76388 and Q77619-32)
CC   or RNA (Q76390 and Q77647-60) directed against the sense strand of the
CC   gene encoding tenascin.  The polynucleotides are based on the
CC   complementary sequence (Q76386) of the consensus mRNA initiation site
CC   sequence (Q77661) for the tenascin gene.  Tenascin is an extracellular
CC   matrix glycoprotein consisting six disulphide-linked subunits, each
CC   having molecular mass of 190-250 kDa.  Tenascin may be important for
CC   smooth muscle cell proliferation as the protein has growth stimulatory
CC   activity.  The polynucleotides can be used to inhibit transcription
CC   of the gene or translation of the mRNA encoding tenascin.  The method is
CC   applicable to a number of diseases where the proliferation of smooth
CC   muscle is involved e.g. vascular stenosis, post-angioplasty restenosis
CC   and other non-angioplasty procedures such as cardiac hypertrophy,
CC   vascular surgery and organ transplant.
XX
SQ   Sequence 21 BP; 4 A; 5 C; 8 G; 4 U; 0 other;

  Query Match             100.0%;  Score 11;  DB 15;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 agtcatggccc 11
           ||||||||||| |
Db      15 AGTCATGGCCC 5


RESULT  14
Q77628/c
ID   Q77628 standard; DNA; 21 BP.
XX
AC   Q77628;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Antisense polynucleotide binds to tenascin gene consensus at -3-+18.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..21
FT                   /*tag=  a
```

```
FT                  /note= "phosphodiester bonds between nucleotides
FT                         may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 10; Page 46; 64pp; English.
XX
CC   A series of antisense polynucleotides, either DNA (Q76388 and Q77619-32)
CC   or RNA (Q76390 and Q77647-60) directed against the sense strand of the
CC   gene encoding tenascin.  The polynucleotides are based on the
CC   complementary sequence (Q76386) of the consensus mRNA initiation site
CC   sequence (Q77661) for the tenascin gene.  Tenascin is an extracellular
CC   matrix glycoprotein consisting six disulphide-linked subunits, each
CC   having molecular mass of 190-250 kDa.  Tenascin may be important for
CC   smooth muscle cell proliferation as the protein has growth stimulatory
CC   activity.  The polynucleotides can be used to inhibit transcription
CC   of the gene or translation of the mRNA encoding tenascin.  The method is
CC   applicable to a number of diseases where the proliferation of smooth
CC   muscle is involved e.g. vascular stenosis, post-angioplasty restenosis
CC   and other non-angioplasty procedures such as cardiac hypertrophy,
CC   vascular surgery and organ transplant.
XX
SQ   Sequence 21 BP; 5 A; 6 C; 7 G; 3 T; 0 other;


  Query Match             100.0%;  Score 11;  DB 15;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 agtcatggccc 11
          ||||||||||| 
Db     18 AGTCATGGCCC 8


RESULT  15
Q77630/c
ID   Q77630 standard; DNA; 21 BP.
XX
AC   Q77630;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Antisense polynucleotide binds to tenascin gene consensus at +1-+21.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..21
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                          may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 10; Page 46; 64pp; English.
XX
CC   A series of antisense polynucleotides, either DNA (Q76388 and Q77619-32)
CC   or RNA (Q76390 and Q77647-60) directed against the sense strand of the
CC   gene encoding tenascin.  The polynucleotides are based on the
CC   complementary sequence (Q76386) of the consensus mRNA initiation site
CC   sequence (Q77661) for the tenascin gene.  Tenascin is an extracellular
CC   matrix glycoprotein consisting six disulphide-linked subunits, each
CC   having molecular mass of 190-250 kDa.  Tenascin may be important for
CC   smooth muscle cell proliferation as the protein has growth stimulatory
CC   activity.  The polynucleotides can be used to inhibit transcription
CC   of the gene or translation of the mRNA encoding tenascin.  The method is
CC   applicable to a number of diseases where the proliferation of smooth
CC   muscle is involved e.g. vascular stenosis, post-angioplasty restenosis
CC   and other non-angioplasty procedures such as cardiac hypertrophy,
CC   vascular surgery and organ transplant.
XX
SQ   Sequence 21 BP; 4 A; 5 C; 8 G; 4 T; 0 other;


  Query Match             100.0%;  Score 11;  DB 15;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 agtcatggccc 11
          ||||||||||| 
Db     15 AGTCATGGCCC 5


Search completed: March 23, 2001, 16:04:40
Job time: 35939 sec
```

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 23, 2001, 06:05:41 ; Search time 551.33 Seconds
(without alignments)
11.583 Million cell updates/sec

Title: US-09-554-267-2
Perfect score: 17
Sequence: 1 ggtggaggtgggtttgg 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 624296

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_36:*
1: /cgn2_2/gcgdata/geneseq/geneseqn/NA1980.DAT:*
2: /cgn2_2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
3: /cgn2_2/gcgdata/geneseq/geneseqn/NA1982.DAT:*
4: /cgn2_2/gcgdata/geneseq/geneseqn/NA1983.DAT:*
5: /cgn2_2/gcgdata/geneseq/geneseqn/NA1984.DAT:*
6: /cgn2_2/gcgdata/geneseq/geneseqn/NA1985.DAT:*
7: /cgn2_2/gcgdata/geneseq/geneseqn/NA1986.DAT:*
8: /cgn2_2/gcgdata/geneseq/geneseqn/NA1987.DAT:*
9: /cgn2_2/gcgdata/geneseq/geneseqn/NA1988.DAT:*
10: /cgn2_2/gcgdata/geneseq/geneseqn/NA1989.DAT:*
11: /cgn2_2/gcgdata/geneseq/geneseqn/NA1990.DAT:*
12: /cgn2_2/gcgdata/geneseq/geneseqn/NA1991.DAT:*
13: /cgn2_2/gcgdata/geneseq/geneseqn/NA1992.DAT:*
14: /cgn2_2/gcgdata/geneseq/geneseqn/NA1993.DAT:*
15: /cgn2_2/gcgdata/geneseq/geneseqn/NA1994.DAT:*
16: /cgn2_2/gcgdata/geneseq/geneseqn/NA1995.DAT:*
17: /cgn2_2/gcgdata/geneseq/geneseqn/NA1996.DAT:*
18: /cgn2_2/gcgdata/geneseq/geneseqn/NA1997.DAT:*
19: /cgn2_2/gcgdata/geneseq/geneseqn/NA1998.DAT:*
20: /cgn2_2/gcgdata/geneseq/geneseqn/NA1999.DAT:*
21: /cgn2_2/gcgdata/geneseq/geneseqn/NA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	14.4	84.7	35	13	Q33260	Triplex forming ol
	2	13.8	81.2	28	14	Q41911	erb B2/neu promote
	3	13.8	81.2	30	14	Q42290	PCR primer SCFV-5
	4	13.8	81.2	30	16	Q92362	PCR primer SCFV-5
	5	13.8	81.2	49	14	Q42288	PCR primer SCFV-2
	6	13.8	81.2	49	16	Q76157	he3 V/J kappa PCR
	7	13.8	81.2	49	16	Q92360	PCR primer SCFV-2
	8	13.8	81.2	49	19	V31091	He3 SCA and geloni
	9	13.8	81.2	49	19	V31093	He3 SCA and geloni
	10	13.8	81.2	50	16	Q76155	he3 heavy chain V/
	11	13.4	78.8	22	19	V51875	Zea mays genome re
c	12	13	76.5	28	19	V31090	He3 SCA and geloni
c	13	13	76.5	49	14	Q42293	PCR primer SCFV-4
c	14	13	76.5	49	16	Q76160	he3 V/J gamma PCR
c	15	13	76.5	49	16	Q92365	PCR primer SCFV-4
	16	12.8	75.3	17	17	T35238	Natural killer lyt
c	17	12.8	75.3	20	19	V40285	Rat equilibrative
c	18	12.8	75.3	21	17	T38149	Primer Y for DNA p
	19	12.8	75.3	25	18	T66196	HCV type 1b ISDR p
	20	12.8	75.3	25	20	Z09394	HCV-1b ISD core re
	21	12.8	75.3	26	20	X40765	Oligonucleotide us
	22	12.8	75.3	26	20	X40774	Oligonucleotide us
c	23	12.8	75.3	29	17	T38184	17y. AccY Prinker
c	24	12.8	75.3	29	17	T38188	19y. SalY Prinker
c	25	12.8	75.3	29	17	T38190	20y. ApaLY Prinker
c	26	12.8	75.3	29	17	T38194	22y. AflY Prinker
c	27	12.8	75.3	29	17	T38168	9y. SgrY Prinker (
c	28	12.8	75.3	29	17	T38172	11y. XbaY Prinker
c	29	12.8	75.3	29	17	T38174	12y. BamY Prinker
c	30	12.8	75.3	29	17	T38178	14y. NotY Prinker
c	31	12.8	75.3	29	17	T38152	1y. EcoY Prinker (
c	32	12.8	75.3	29	17	T38158	4y. HinY Prinker (
c	33	12.8	75.3	29	17	T38164	7y. NcoY Prinker (
c	34	12.8	75.3	30	17	T38170	10y. AscY Prinker
c	35	12.8	75.3	31	17	T38176	13y. PacY Prinker
c	36	12.8	75.3	31	17	T38180	15y. SacIIY Prinke
c	37	12.8	75.3	31	17	T38154	2y. ClaY Prinker (
c	38	12.8	75.3	31	17	T38162	6y. AseY Prinker (
c	39	12.8	75.3	33	17	T38182	16y. ApaY Prinker
c	40	12.8	75.3	33	17	T38186	18y. KpnY Prinker
c	41	12.8	75.3	33	17	T38192	21y. PstY Prinker
c	42	12.8	75.3	33	17	T38166	8y. SphY Prinker (
c	43	12.8	75.3	33	17	T38156	3y. AatY Prinker (
c	44	12.8	75.3	33	17	T38160	5y. SacY Prinker (
	45	12.8	75.3	36	11	Q04999	Sequence binding t

ALIGNMENTS

RESULT 1
Q33260
ID Q33260 standard; DNA; 35 BP.
XX
AC Q33260;
XX
DT 04-MAY-1993 (first entry)
XX
DE Triplex forming oligonucleotide #3 - binds to EGFR promoter region.
XX
KW Triple helix; modified bases; modified DNA bases;
KW modified 2'-deoxyribonucleoside; triplex forming oligonucleotide;
KW HIV; AIDS; regulate gene expression; hormone regulation; antisense;
KW ss.
XX
OS Synthetic.
XX
PN WO9221690-A.
XX
PD 10-DEC-1992.
XX
PF 04-JUN-1992; 92WO-US04795.
XX
PR 05-JUN-1991; 91US-0712151.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (TRIP-) TRIPLEX PHARM CORP.
XX
PI Hogan ME, Rao TS, Revankar GR, Shroff HN;
XX
DR WPI; 1992-433604/52.
XX
PT New purine base modified 2'-deoxyribonucleoside(s) - and
PT triplex-forming oligonucleotide(s) contg. them, inhibit HIV-1 and
PT regulate gene expression

```
XX
PS   Example 23; Page 35a; 72pp; English.
XX
CC   This sequence is used to demonstrate stressed triplet formation of
CC   sites of TA and GC inversion. Together with Q33254,5 it forms a
CC   triple helix. It contains chemically modified 2'-deoxyribonucleosides.
CC   Triplex forming oligonucleotides like this may be used for treating
CC   a variety of diseases, including AIDS, and for the regulation of
CC   proteins, hormones, and gene expression as antisense
CC   oligonucleotides.
XX
SQ   Sequence 35 BP; 0 A; 0 C; 20 G; 15 T; 0 other;


  Query Match             84.7%;  Score 14.4;  DB 13;  Length 35;
  Best Local Similarity   93.8%;  Pred. No. 3.4e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 ggtggaggtgggtttg 16
          ||||| ||||||||||
Db      8 ggtggtggtgggtttg 23


RESULT   2
Q41911
ID   Q41911 standard; DNA; 28 BP.
XX
AC   Q41911;
XX
DT   30-SEP-1993  (first entry)
XX
DE   erb B2/neu promoter randomised isomer NEUctr.
XX
KW   Purine; promoter; human; erb B2/neu; gene; HER-2; homologue; rat; neu;
KW   triplex-forming oligonucleotide; TFO; retinoic acid; transgenic mice;
KW   core promoter element; growth factor; c-AMP; cancer; mammary tumour;
KW   tumour; NIH3T3 cells; pyrimidine; TPA; major groove; target; CAT box;
KW   TATA box; transcription; transforming; AT box protein; RNA polymerase;
KW   TFIId; control isomer; expression; ss.
XX
OS   Synthetic.
XX
PN   WO9309788-A.
XX
PD   27-MAY-1993.
XX
PF   28-OCT-1992;   92WO-US09202.
XX
PR   13-NOV-1991;   91US-0792319.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI   Hogan ME;
XX
DR   WPI; 1993-182231/22.
XX
PT   Use of triplex-forming oligo-nucleotide - to inhibit
PT   proliferation of cells contg. an erb. B2/neu gene site, for
PT   treating cancers, psoriasis etc.
XX
PS   Disclosure; Page 10; 26pp; English.
XX
CC   The sequences given in Q41911-13 are control isomers which comprise
CC   randomised sequences, based on triplex-forming isomers (TFO), which
CC   do not bind to the erb B2/neu target sequence, and have no effect
CC   on erb B2/neu expression. The erb B2/neu (HER-2) gene is the human
CC   homologue of the rat neu gene. This human homologue is frequently
CC   amplified in tumours. When expressed at high levels in NIH3T3 cells,
CC   erb B2/neu is strongly transforming and results in a high incidence
CC   of mammary tumours in transgenic mice. The core promoter element of
CC   erb B2/neu resides within a 300 bp region of the 5' flanking domain.
CC   This region contains elements which confer sensitivity to enhance
CC   promoter function in the presence of cell growth factors such as TPA,
CC   c-AMP and retinoic acid. Therefore, overexpression of of erb B2/neu
CC   may be one mechanism leading to cancer initiation or expression. The
CC   sequences given in Q41905-10 are TFOs which are specific to the
CC   promoter region of erb B2/neu. They bind to the major groove of the
CC   DNA duplex to form a triplex. The TFOs are complementary to the
CC   target sequence such they include a G when the complentary location
CC   in the DNA duplex is a GC pair and T when the complementary location
CC   in the duplex DNA is an AT base pair. The target site for these TFOs
CC   should have a stretch of DNA which is at least 65% purine or
CC   pyrimidine bases. The long purine run in the erb B2/neu promoter
CC   region includes the CAT box and the TATA box. Inhibition at the CAT
CC   box will inhibit transcription initiation by interfering directly with
CC   the CAT box protein-RNA polymerase interaction. Further inhibition of
CC   the protein binding at the CAT box site can also block the interaction
CC   of the CAT protein with TFIId at the TATA box. Inhibition of the erb
CC   B2/neu promoter region by the TFOs may be used to inhibit expression
CC   of the gene and may therefore be used to treat or prevent cancers.
XX
SQ   Sequence 28 BP; 0 A; 0 C; 18 G; 10 T; 0 other;


  Query Match             81.2%;  Score 13.8;  DB 14;  Length 28;
  Best Local Similarity   88.2%;  Pred. No. 6.2e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 ggtggaggtgggtttgg 17
          ||||| ||||||| |||
Db      1 ggtggtggtgggtgtgg 17


RESULT   3
Q42290
ID   Q42290 standard; cDNA; 30 BP.
XX
AC   Q42290;
XX
DT   13-SEP-1993  (first entry)
XX
DE   PCR primer SCFV-5 to amplify he3 V/J kappa sequences.
XX
KW   Type I ribosome-inactivating protein; ricin; gelonin;
KW   immunoconjugate; autoimmune disease; cell killing; toxin;
KW   overlap extension polymerase chain reaction; H65 variable region;
KW   RMA; rabbit muscle aldolase; cathepsin cleavage;
KW   SLT; E.coli Shiga-like toxin; human engineered antibody; ss.
XX
OS   Synthetic.
XX
PN   WO9309130-A.
XX
PD   13-MAY-1993.
XX
PF   04-NOV-1992;   92WO-US09487.
XX
PR   04-NOV-1991;   91US-0787567.
PR   19-JUN-1992;   92US-0901707.
XX
PA   (XOMA ) XOMA CORP.
XX
PI   Berhard SL,  Better MD,  Carroll SF,  Lane JA,  Lei SP;
XX
DR   WPI; 1993-167617/20.
XX
PT   Analogues of type I ribosome inactivating protein - useful as
PT   cytotoxic agents, immuno toxins for treating auto immune diseases,
PT   cancer, graft versus host disease and selective cell killing in=vivo
XX
PS   Example 12; Page 76; 163pp; English.
XX
CC   Primers SCFV-5 and SCFV-6 (Q42290 and Q42291, respectively) were
CC   used to amplify a 367bp DNA fragment contg. the he3 V/J kappa
CC   sequences from pING4627. Concurrently, primers H65-G3 and SCFV-4
CC   (Q42292 and Q42293, respectively) were used to amplify a he3 heavy
```

CC chain V/J gamma segment from pING4623, generating a 385bp fragment.
CC The products from these reactions were mixed and amplified by
CC outside primers H65-G3 and SCFV-6. The single chain antibody form
CC of the he3 H65 variable domain assembled in this way was used to
CC make two fusion constructs in which the natural sequence gelonin
CC gene was positioned at the N-terminus and the SLT or RMA linker
CC peptide was positioned between the gelonin and scAb domains.
XX
SQ Sequence 30 BP; 4 A; 3 C; 17 G; 6 T; 0 other;

Query Match 81.2%; Score 13.8; DB 14; Length 30;
Best Local Similarity 88.2%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ggtggaggtgggtttgg 17
||||||||||||| ||
Db 1 ggtggaggtgggtccgg 17

RESULT 4
Q92362
ID Q92362 standard; DNA; 30 BP.
XX
AC Q92362;
XX
DT 01-JAN-1996 (first entry)
XX
DE PCR primer SCFV-5 for amplifying he3 V/J kappa sequences.
XX
KW he3; V/J; kappa chain; PCR primer; ss.
XX
OS Synthetic.
XX
PN US5416202-A.
XX
PD 16-MAY-1995.
XX
PF 09-DEC-1992; 92US-0988430.
XX
PR 09-DEC-1992; 92US-0988430.
PR 04-NOV-1991; 91US-0787567.
XX
PA (XOMA) XOMA CORP.
XX
PI Bernhard SL, Better MD, Carroll SF, Lane JA, Lei SP;
XX
DR WPI; 1995-193480/25.
XX
PT Polynucleotide(s) encoding gelonin analogues - having a cystein
PT residue for intermolecular bonding for the prodn. of immuno-toxins(s)
XX
PS Example; Column 46; 66pp; English.
XX
CC The scAb V-J gamma::[(Gly)4-Ser]::V-Jkappa was assembled by
CC amplification with primers SCFV-5 and SCFV-6 generating a 367 bp
CC fragment contg. the he3 V/J kappa sequences. Primers H65-G3 and
CC SCFV-4 generated a 385 bp fragment contg. he3 gamma V/J sequences
CC by PCR. The products from these reactions were mixed and amplified
CC with H65-G3 and SCFV-6. The 737 bp product was treated with T4
CC polymerase and cut with XhoI. Ligation into pING3755 and pING3748
CC resulted in assembly of the Gelonin::RMA::scAB
CC V-JGamma::[(Gly)4Ser]3::V-Jkappa gene fusion in pING3638 and
CC Gelonin::SLT::scAb V-JGamma[(Gly)4Ser]3::V-Jkappa gene fusion in
CC pING4639, respectively.
XX
SQ Sequence 30 BP; 4 A; 3 C; 17 G; 6 T; 0 other;

Query Match 81.2%; Score 13.8; DB 16; Length 30;
Best Local Similarity 88.2%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ggtggaggtgggtttgg 17
||||||||||||| ||
Db 1 ggtggaggtgggtccgg 17

RESULT 5
Q42288
ID Q42288 standard; cDNA; 49 BP.
XX
AC Q42288;
XX
DT 13-SEP-1993 (first entry)
XX
DE PCR primer SCFV-2 to amplify he3 V/J gamma sequences.
XX
KW Type I ribosome-inactivating protein; ricin; gelonin;
KW immunoconjugate; autoimmune disease; cell killing; toxin;
KW overlap extension polymerase chain reaction; H65 variable region;
KW RMA; rabbit muscle aldolase; cathepsin cleavage; heavy chain;
KW SLT; E.coli Shiga-like toxin; human engineered antibody; ss.
XX
OS Synthetic.
XX
PN WO9309130-A.
XX
PD 13-MAY-1993.
XX
PF 04-NOV-1992; 92WO-US09487.
XX
PR 04-NOV-1991; 91US-0787567.
PR 19-JUN-1992; 92US-0901707.
XX
PA (XOMA) XOMA CORP.
XX
PI Berhard SL, Better MD, Carroll SF, Lane JA, Lei SP;
XX
DR WPI; 1993-167617/20.
XX
PT Analogues of type I ribosome inactivating protein - useful as
PT cytotoxic agents, immuno toxins for treating auto immune diseases,
PT cancer, graft versus host disease and selective cell killing in-vivo
XX
PS Example 12; Page 75; 163pp; English.
XX
CC Primers SCFV-1 and HUK-7 (Q42286 and Q42287, respectively) were
CC used to amplify a 352bp DNA fragment contg. the he3 V/J kappa
CC sequences from pING4627. Concurrently, primers SCFV-2 and SCFV-3
CC (Q42288 and Q42289, respectively) were used to amplify a he3 heavy
CC chain V/J gamma segment from pING4623, generating a 400bp fragment.
CC The products from these reactions were mixed and amplified by
CC outside primers HUK-7 and SCFV-3. The single chain antibody form
CC of the he3 H65 variable domain assembled in this way was used to
CC make two fusion constructs in which the natural sequence gelonin
CC gene was positioned at the N-terminus and the SLT or RMA linker
CC peptide was positioned between the gelonin and scAb domains.
XX
SQ Sequence 49 BP; 8 A; 6 C; 24 G; 11 T; 0 other;

Query Match 81.2%; Score 13.8; DB 14; Length 49;
Best Local Similarity 88.2%; Pred. No. 6.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ggtggaggtgggtttgg 17
||||||||||||| ||
Db 1 ggtggaggtgggtccgg 17

RESULT 6
Q76157
ID Q76157 standard; DNA; 49 BP.
XX
AC Q76157;

```
XX
DT   28-JUL-1995  (first entry)
XX
DE   he3 V/J kappa PCR primer SCFV-5.
XX
KW   cytotoxic therapeutic agents; autoimmune disease; cancer;
KW   graft-versus-host disease; he3 V/J kappa; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO9426910-A.
XX
PD   24-NOV-1994.
XX
PF   12-MAY-1994;   94WO-US05348.
XX
PR   12-MAY-1993;   93US-0064691.
XX
PA   (XOMA ) XOMA CORP.
XX
PI   Better MD,  Carroll SS,  Studnicka GM,  Carroll SF;
XX
DR   WPI; 1995-006804/01.
XX
PT   Polynucleotide(s) encoding type I ribosome-inactivating proteins
PT   - which are suitable for use as components of cytotoxic
PT   therapeutic agents.
XX
PS   Example 16; Page 106; 221pp; English.
XX
CC   Q76157 and Q76158 are a pair of primers for the PCR amplification
CC   of the he3 V/J kappa region, they were used in the construction of
CC   a cytotoxic therapeutic agent (CTA), immunoconjugate. CTAs can be
CC   used in the treatment of diseases where the elimination of a
CC   particular cell type is desired, such as autoimmune disease, cancer
CC   and graft-versus-host disease.
XX
SQ   Sequence 49 BP; 10 A; 8 C; 21 G; 10 T; 0 other;


  Query Match             81.2%;  Score 13.8;  DB 16;  Length 49;
  Best Local Similarity   88.2%;  Pred. No. 6.3e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 ggtggaggtgggtttgg 17
          ||||||||||||  ||
Db      1 ggtggaggtgggtccgg 17


RESULT   7
Q92360
ID   Q92360 standard; DNA; 49 BP.
XX
AC   Q92360;
XX
DT   01-JAN-1996  (first entry)
XX
DE   PCR primer SCFV-2 for amplifying he3 heavy chain V/J gamma segment.
XX
KW   he3; V/J; heavy chain; gamma segment; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   US5416202-A.
XX
PD   16-MAY-1995.
XX
PF   09-DEC-1992;   92US-0988430.
XX
PR   09-DEC-1992;   92US-0988430.
PR   04-NOV-1991;   91US-0787567.
XX
PA   (XOMA ) XOMA CORP.
XX
PI   Bernhard SL,  Better MD,  Carroll SF,  Lane JA,  Lei SP;
XX
DR   WPI; 1995-193480/25.
XX
PT   Polynucleotide(s) encoding gelonin analogues - having a cystein
PT   residue for intermolecular bonding for the prodn. of immuno-toxins(s)
XX
PS   Example; Column 46; 66pp; English.
XX
CC   For assembly of the scAb segment V-J kappa::[(Gly)4-Ser]::V-J
CC   gamma, primers HUK-7 and SCFV-1 were used to amplify a 352 bp DNA
CC   fragment contg. he3 V/J kappa sequences. Concurrently, primers
CC   SCFV-2 and SCFV-3 were used to amplify a he3 heavy chain V/J
CC   gamma segment, generating a 400 bp fragment.
XX
SQ   Sequence 49 BP; 8 A; 6 C; 24 G; 11 T; 0 other;


  Query Match             81.2%;  Score 13.8;  DB 16;  Length 49;
  Best Local Similarity   88.2%;  Pred. No. 6.3e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 ggtggaggtgggtttgg 17
          ||||||||||||  ||
Db      1 ggtggaggtgggtccgg 17


RESULT   8
V31091
ID   V31091 standard; DNA; 49 BP.
XX
AC   V31091;
XX
DT   18-AUG-1998  (first entry)
XX
DE   He3 SCA and gelonin-SCA fusion protein construction PCR primer SCFV-2.
XX
KW   Humanised; human; mouse; CD5; anti-CD5 antibody; immunoglobulin;
KW   depletion; cytotoxic; immunoconjugate; fusion protein; psoriasis;
KW   autoimmune disease; rheumatoid arthritis; type I diabetes;
KW   PCR primer; ss.
XX
OS   Synthetic.
XX
PN   US5770196-A.
XX
PD   23-JUN-1998.
XX
PF   07-JUN-1995;   95US-0472788.
XX
PR   23-JUN-1993;   93US-0082842.
PR   13-DEC-1991;   91US-0808464.
PR   14-DEC-1992;   92WO-US10906.
PR   07-JUN-1995;   95US-0472788.
XX
PA   (XOMA ) XOMA CORP.
XX
PI   Studnicka GM;
XX
DR   WPI; 1998-376744/32.
XX
PT   Depletion of CD5-positive cells in vivo - using anti-CD5 antibodies
PT   with humanised variable regions
XX
PS   Example 12; Column 37; 77pp; English.
XX
CC   A method has been developed of depleting CD5+ cells in an animal. The
CC   method comprises administering a cytotoxic protein containing a modified
CC   immunoglobulin (Ig) variable domain, where the protein is an anti-CD5 Ig
CC   molecule or an immunoconjugate or fusion protein containing an anti-CD5
CC   Ig molecule, and where the modified Ig variable domain comprises at
CC   least one of (a) a modified light chain variable region (see W58473 or
```

```
CC   W58480), and (b) a modified heavy chain variable region (see W58479 or
CC   W58481), where W58478 and W58479 are humanised forms of the H65 light
CC   and heavy chain variable domains with low risk amino acid substitutions
CC   [i.e. low risk of reducing antigen-binding specificity.] and W58480 and
CC   W58481 are humanised forms of the H65 light and heavy chain variable
CC   domains with moderate risk amino acid substitutions and are present in
CC   humanised H65 antibody he3 (ATCC HB 11206). The method is useful for
CC   treating autoimmune diseases, especially systemic lupus erythematosus,
CC   rheumatoid arthritis, psoriasis or type I diabetes. The present sequence
CC   represents a PCR primer used in the construction of he3 single chain
CC   antibody (SCA) and gelonin-SCA fusion proteins.
XX
SQ   Sequence 49 BP; 8 A; 6 C; 24 G; 11 T; 0 other;


  Query Match             81.2%;  Score 13.8;  DB 19;  Length 49;
  Best Local Similarity   88.2%;  Pred. No. 6.3e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 ggtggaggtgggtttgg 17
          |||||||||||||  ||
Db      1 ggtggaggtgggtccgg 17


RESULT   9
V31093
ID   V31093 standard; DNA; 49 BP.
XX
AC   V31093;
XX
DT   18-AUG-1998  (first entry)
XX
DE   He3 SCA and gelonin-SCA fusion protein construction PCR primer SCFV-5.
XX
KW   Humanised; human; mouse; CD5; anti-CD5 antibody; immunoglobulin;
KW   depletion; cytotoxic; immunoconjugate; fusion protein; psoriasis;
KW   autoimmune disease; rheumatoid arthritis; type I diabetes;
KW   PCR primer; ss.
XX
OS   Synthetic.
XX
PN   US5770196-A.
XX
PD   23-JUN-1998.
XX
PF   07-JUN-1995;   95US-0472788.
XX
PR   23-JUN-1993;   93US-0082842.
PR   13-DEC-1991;   91US-0808464.
PR   14-DEC-1992;   92WO-US10906.
PR   07-JUN-1995;   95US-0472788.
XX
PA   (XOMA ) XOMA CORP.
XX
PI   Studnicka GM;
XX
DR   WPI; 1998-376744/32.
XX
PT   Depletion of CD5-positive cells in vivo - using anti-CD5 antibodies
PT   with humanised variable regions
XX
PS   Example 12; Column 38; 77pp; English.
XX
CC   A method has been developed of depleting CD5+ cells in an animal. The
CC   method comprises administering a cytotoxic protein containing a modified
CC   immunoglobulin (Ig) variable domain, where the protein is an anti-CD5 Ig
CC   molecule or an immunoconjugate or fusion protein containing an anti-CD5
CC   Ig molecule, and where the modified Ig variable domain comprises at
CC   least one of (a) a modified light chain variable region (see W58478 or
CC   W58480), and (b) a modified heavy chain variable region (see W58479 or
CC   W58481), where W58478 and W58479 are humanised forms of the H65 light
CC   and heavy chain variable domains with low risk amino acid substitutions
CC   [i.e. low risk of reducing antigen-binding specificity.] and W58480 and
CC   W58481 are humanised forms of the H65 light and heavy chain variable
CC   domains with moderate risk amino acid substitutions and are present in
CC   humanised H65 antibody he3 (ATCC HB 11206). The method is useful for
CC   treating autoimmune diseases, especially systemic lupus erythematosus,
CC   rheumatoid arthritis, psoriasis or type I diabetes. The present sequence
CC   represents a PCR primer used in the construction of he3 single chain
CC   antibody (SCA) and gelonin-SCA fusion proteins.
XX
SQ   Sequence 49 BP; 10 A; 8 C; 21 G; 10 T; 0 other;


  Query Match             81.2%;  Score 13.8;  DB 19;  Length 49;
  Best Local Similarity   88.2%;  Pred. No. 6.3e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 ggtggaggtgggtttgg 17
          |||||||||||||  ||
Db      1 ggtggaggtgggtccgg 17


RESULT  10
Q76155
ID   Q76155 standard; DNA; 50 BP.
XX
AC   Q76155;
XX
DT   28-JUL-1995  (first entry)
XX
DE   he3 heavy chain V/J gamma PCR primer SCFV-2.
XX
KW   cytotoxic therapeutic agents; autoimmune disease; cancer;
KW   graft-versus-host disease; he3 heavy chain V/J gamma; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO9426910-A.
XX
PD   24-NOV-1994.
XX
PF   12-MAY-1994;   94WO-US05348.
XX
PR   12-MAY-1993;   93US-0064691.
XX
PA   (XOMA ) XOMA CORP.
XX
PI   Better MD,  Carroll SS,  Studnicka GM,  Carroll SF;
XX
DR   WPI; 1995-006804/01.
XX
PT   Polynucleotide(s) encoding type I ribosome-inactivating proteins
PT   - which are suitable for use as components of cytotoxic
PT   therapeutic agents.
XX
PS   Example 16; Page 106; 221pp; English.
XX
CC   Q76155 and Q76156 are a pair of primers for the PCR amplification
CC   of the he3 heavy chain V/J gamma region, they were used in the
CC   construction of a cytotoxic therapeutic agent (CTA), immunoconjugate.
CC   CTAs can be used in the treatment of diseases where the elimination
CC   of a particular cell type is desired, such as autoimmune disease,
CC   cancer and graft-versus-host
CC   disease.
XX
SQ   Sequence 50 BP; 9 A; 6 C; 24 G; 11 T; 0 other;


  Query Match             81.2%;  Score 13.8;  DB 16;  Length 50;
  Best Local Similarity   88.2%;  Pred. No. 6.3e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 ggtggaggtgggtttgg 17
          |||||||||||||  ||
Db      1 ggtggaggtgggtccgg 17
```

```
RESULT  11
V51875
ID   V51875 standard; DNA; 22 BP.
XX
AC   V51875;
XX
DT   02-FEB-1999  (first entry)
XX
DE   Zea mays genome reverse PCR primer #171.
XX
KW   Polymorphic marker; allele-specific; probe; amplification; PCR primer;
KW   hybridisation; plant; hybrid certification; genetic contribution;
KW   progeny; back-cross; hybrid; ancestry; corn; ss.
XX
OS   Synthetic.
OS   Zea mays.
XX
PN   WO9824796-A1.
XX
PD   11-JUN-1998.
XX
PF   01-DEC-1997;   97WO-US21782.
XX
PR   07-MAR-1997;   97US-0813507.
PR   02-DEC-1996;   96US-0032069.
XX
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Landry BS,  Lemieux B,  Murigneux A,  Sapolsky RJ;
XX
DR   WPI; 1998-333252/29.
XX
PT   Brassica species allele-specific oligonucleotide probes and primers
PT   - useful for plant breeding
XX
PS   Example 1; Page Page 53; 65pp; English.
XX
CC   V51705-V52008 are reverse PCR primers used to amplify fragments of the
CC   Zea mays genome in order to detect polymorphic markers. Such markers can
CC   be used in the construction of allele-specific primers and probes for
CC   amplification or hybridisation, e.g. to determine common or disparate
CC   ancestry between 2 or more plants, to monitor the genetic contribution
CC   of an ancestral plant, to trace the progeny of proprietary plants, in
CC   certification of a hybrid plant or to identify the progeny of a
CC   back-crossed plant with an ancestral plant.
XX
SQ   Sequence 22 BP; 4 A; 2 C; 10 G; 6 T; 0 other;


  Query Match             78.8%;  Score 13.4;  DB 19;  Length 22;
  Best Local Similarity   93.3%;  Pred. No. 9.3e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 ggtggaggtgggttt 15
          ||||||||||| ||
Db      1 ggtggaggtggggtt 15


RESULT  12
V31090/c
ID   V31090 standard; DNA; 28 BP.
XX
AC   V31090;
XX
DT   18-AUG-1998  (first entry)
XX
DE   He3 SCA and gelonin-SCA fusion protein construction PCR primer SCFV-1.
XX
KW   Humanised; human; mouse; CD5; anti-CD5 antibody; immunoglobulin;
KW   depletion; cytotoxic; immunoconjugate; fusion protein; psoriasis;
KW   autoimmune disease; rheumatoid arthritis; type I diabetes;
KW   PCR primer; ss.
XX
OS   Synthetic.
XX
PN   US5770196-A1.
XX
PD   23-JUN-1998.
XX
PF   07-JUN-1995;   95US-0472788.
XX
PR   23-JUN-1993;   93US-0082842.
PR   13-DEC-1991;   91US-0808464.
PR   14-DEC-1992;   92WO-US10906.
PR   07-JUN-1995;   95US-0472788.
XX
PA   (XOMA ) XOMA CORP.
XX
PI   Studnicka GM;
XX
DR   WPI; 1998-376744/32.
XX
PT   Depletion of CD5-positive cells in vivo - using anti-CD5 antibodies
PT   with humanised variable regions
XX
PS   Example 12; Column 37; 77pp; English.
XX
CC   A method has been developed of depleting CD5+ cells in an animal. The
CC   method comprises administering a cytotoxic protein containing a modified
CC   immunoglobulin (Ig) variable domain, where the protein is an anti-CD5 Ig
CC   molecule or an immunoconjugate or fusion protein containing an anti-CD5
CC   Ig molecule, and where the modified Ig variable domain comprises at
CC   least one of (a) a modified light chain variable region (see W58479 or
CC   W58480), and (b) a modified heavy chain variable region (see W58479 or
CC   W58481), where W58478 and W58479 are humanised forms of the H65 light
CC   and heavy chain variable domains with low risk amino acid substitutions
CC   [i.e. low risk of reducing antigen-binding specificity.] and W58480 and
CC   W58481 are humanised forms of the H65 light and heavy chain variable
CC   domains with moderate risk amino acid substitutions and are present in
CC   humanised H65 antibody he3 (ATCC HB 11206). The method is useful for
CC   treating autoimmune diseases, especially systemic lupus erythematosus,
CC   rheumatoid arthritis, psoriasis or type I diabetes. The present sequence
CC   represents a PCR primer used in the construction of he3 single chain
CC   antibody (SCA) and gelonin-SCA fusion proteins.
XX
SQ   Sequence 28 BP; 7 A; 15 C; 4 G; 2 T; 0 other;


  Query Match             76.5%;  Score 13;  DB 19;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggtggaggtgggt 13
          |||||||||||||
Db     16 GGTGGAGGTGGGT 4


RESULT  13
Q42293/c
ID   Q42293 standard; cDNA; 49 BP.
XX
AC   Q42293;
XX
DT   13-SEP-1993  (first entry)
XX
DE   PCR primer SCFV-4 to amplify he3 V/J gamma sequences.
XX
KW   Type I ribosome-inactivating protein; ricin; gelonin;
KW   immunoconjugate; autoimmune disease; cell killing; toxin;
KW   overlap extension polymerase chain reaction; H65 variable region;
KW   RMA; rabbit muscle aldolase; cathepsin cleavage; heavy chain;
KW   SLT; E.coli Shiga-like toxin; human engineered antibody; ss.
XX
OS   Synthetic.
```

XX
PN WO9309130-A.
XX
PD 13-MAY-1993.
XX
PF 04-NOV-1992; 92WO-US09487.
XX
PR 04-NOV-1991; 91US-0787567.
PR 19-JUN-1992; 92US-0901707.
XX
PA (XOMA) XOMA CORP.
XX
PI Berhard SL, Better MD, Carroll SF, Lane JA, Lei SP;
XX
DR WPI; 1993-167617/20.
XX
PT Analogues of type I ribosome inactivating protein - useful as
PT cytotoxic agents, immuno toxins for treating auto immune diseases,
PT cancer, graft versus host disease and selective cell killing in=vivo
XX
PS Example 12; Page 76; 163pp; English.
XX
CC Primers SCFV-5 and SCFV-6 (Q42290 and Q42291, respectively) were
CC used to amplify a 367bp DNA fragment contg. the he3 V/J kappa
CC sequences from pING4627. Concurrently, primers H65-G3 and SCFV-4
CC (Q42292 and Q42293, respectively) were used to amplify a he3 heavy
CC chain V/J gamma segment from pING4623, generating a 385bp fragment.
CC The products from these reactions were mixed and amplified by
CC outside primers H65-G3 and SCFV-6. The single chain antibody form
CC of the he3 H65 variable domain assembled in this way was used to
CC make two fusion constructs in which the natural sequence gelonin
CC gene was positioned at the N-terminus and the SLT or RMA linker
CC peptide was positioned between the gelonin and scAb domains.
XX
SQ Sequence 49 BP; 11 A; 21 C; 12 G; 5 T; 0 other;

Query Match 76.5%; Score 13; DB 14; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ggtggaggtgggt 13
||||||||||||| |
Db 16 GGTGGAGGTGGGT 4

RESULT 14
Q76160/c
ID Q76160 standard; DNA; 49 BP.
XX
AC Q76160;
XX
DT 28-JUL-1995 (first entry)
XX
DE he3 V/J gamma PCR primer SCVF-4.
XX
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease; he3 V/J gamma; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO9426910-A.
XX
PD 24-NOV-1994.
XX
PF 12-MAY-1994; 94WO-US05348.
XX
PR 12-MAY-1993; 93US-0064691.
XX
PA (XOMA) XOMA CORP.
XX
PI Better MD, Carroll SS, Studnicka GM, Carroll SF;
XX
DR WPI; 1995-006804/01.
XX
PT Polynucleotide(s) encoding type I ribosome-inactivating proteins
PT - which are suitable for use as components of cytotoxic
PT therapeutic agents.
XX
PS Example 16; Page 107; 221pp; English.
XX
CC Q76159 and Q76160 are a pair of primers for the PCR amplification
CC of the he3 V/J gamma region, they were used in the construction of
CC a cytotoxic therapeutic agent (CTA), immunoconjugate. CTAs can be
CC used in the treatment of diseases where the elimination of a
CC particular cell type is desired, such as autoimmune disease, cancer
CC and graft-versus-host disease.
XX
SQ Sequence 49 BP; 11 A; 21 C; 12 G; 5 T; 0 other;

Query Match 76.5%; Score 13; DB 16; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ggtggaggtgggt 13
||||||||||||| |
Db 16 GGTGGAGGTGGGT 4

RESULT 15
Q92365/c
ID Q92365 standard; DNA; 49 BP.
XX
AC Q92365;
XX
DT 01-JAN-1996 (first entry)
XX
DE PCR primer SCFV-4 for amplifying he3 V/J gamma sequences.
XX
KW he3; V/J; gamma chain; PCR primer; ss.
XX
OS Synthetic.
XX
PN US5416202-A.
XX
PD 16-MAY-1995.
XX
PF 09-DEC-1992; 92US-0988430.
XX
PR 09-DEC-1992; 92US-0988430.
PR 04-NOV-1991; 91US-0787567.
XX
PA (XOMA) XOMA CORP.
XX
PI Bernhard SL, Better MD, Carroll SF, Lane JA, Lei SP;
XX
DR WPI; 1995-193480/25.
XX
PT Polynucleotide(s) encoding gelonin analogues - having a cystein
PT residue for intermolecular bonding for the prodn. of immuno-toxins(s)
XX
PS Example; Column 46; 66pp; English.
XX
CC The scAb V-J gamma::[(Gly)4-Ser]::V-Jkappa was assembled by
CC amplification with primers SCFV-5 and SCFV-6 generating a 367 bp
CC fragment contg. the he3 V/J kappa sequences. Primers H65-G3 and
CC SCFV-4 generated a 385 bp fragment contg. he3 gamma V/J sequences
CC by PCR. The products from these reactions were mixed and amplified
CC with H65-G3 and SCFV-6. The 737 bp product was treated with T4
CC polymerase and cut with XhoI. Ligation into pING3755 and pING3748
CC resulted in assembly of the Gelonin::RMA::scAB
CC V-JGamma::[(Gly)4Ser]3::V-Jkappa gene fusion in pING3638 and
CC Gelonin::SLT::scAb V-JGamma[(Gly)4Ser]3::V-Jkappa gene fusion in
CC pING4639, respectively.
XX

SQ Sequence 49 BP; 11 A; 21 C; 12 G; 5 T; 0 other;

Query Match 76.5%; Score 13; DB 16; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 ggtggaggtgggt 13
           |||||||||||||
Db      16 GGTGGAGGTGGGT 4
```

Search completed: March 23, 2001, 16:04:31
Job time: 35930 sec

```
;    NUMBER OF SEQUENCES:  293
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz & No. 5948611ris
;      STREET:  One Liberty Place - 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  DISKETTE, 3.5 INCH
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows 3.1
;      SOFTWARE:  WORDPERFECT 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/256,426B
;      FILING DATE:  03-FEB-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/10964
;      FILING DATE:  12-NOV-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/977,284
;      FILING DATE:  13-NOV-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mark DeLuca
;      REGISTRATION NUMBER:  33,229
;      REFERENCE/DOCKET NUMBER:  TJU-1082
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-3100
;      TELEFAX:  (215) 568-3439
;  INFORMATION FOR SEQ ID NO:  154:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  SINGLE
;      TOPOLOGY:  LINEAR
;    ANTI-SENSE:  YES
US-08-256-426B-154


  Query Match             87.7%;  Score 11.4;  DB 2;  Length 21;
  Best Local Similarity   92.3%;  Pred. No. 5.7e+02;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 caagaaagacacc 13
           ||||| |||||||
Db       4 CAAGACAGACACC 16


RESULT   5
US-08-444-818-754
; Sequence 754, Application US/08444818
; Patent No. 6150087
;  GENERAL INFORMATION:
;    APPLICANT:  Chien, David Y.
;    APPLICANT:  Rutter, William J.
;    TITLE OF INVENTION:  NANBV Diagnostics and Vaccines
;    NUMBER OF SEQUENCES:  777
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Chiron Corporation
;      STREET:  4560 Horton Street
;      CITY:  Emeryville
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94608-2916
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/444,818
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/403,590
;      FILING DATE:  14-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Harbin, Alisa A.
;      REGISTRATION NUMBER:  33,895
;      REFERENCE/DOCKET NUMBER:  0110.002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (508)359-3876
;      TELEFAX:  (508)359-3885
;  INFORMATION FOR SEQ ID NO:  754:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "primer 156e16B -  derived
;      DESCRIPTION:  from clone 156e"
US-08-444-818-754


  Query Match             84.6%;  Score 11;  DB 3;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 9.2e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 caagaaagaca 11
           ||||||||||
Db       4 CAAGAAAGACA 14


RESULT   6
US-08-629-001A-103/c
; Sequence 103, Application US/08629001A
; Patent No. 5858661
;  GENERAL INFORMATION:
;    APPLICANT:  Shiloh, Yosef
;    TITLE OF INVENTION:  ATAXIA-TELANGIECTASIA GENE AND ITS
;    TITLE OF INVENTION:  GENOMIC ORGANIZATION
;    NUMBER OF SEQUENCES:  139
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Kohn & Associates
;      STREET:  30500 No. 5858661thwestern Hwy.
;      CITY:  Farmington Hills
;      STATE:  Michigan
;      COUNTRY:  US
;      ZIP:  48334
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/629,001A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kohn, Kenneth I.
;      REGISTRATION NUMBER:  30,955
;      REFERENCE/DOCKET NUMBER:  2290.00032
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (810) 539-5050
;      TELEFAX:  (810) 539-5055
;  INFORMATION FOR SEQ ID NO:  103:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  30 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-629-001A-103
```

```
  Query Match             84.6%;  Score 11;  DB 2;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 9.4e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 aagaaagacac 12
          ||||||||||||
Db     18 AAGAAAGACAC 8


RESULT   7
US-08-438-639-15
; Sequence 15, Application US/08438639
; Patent No. 5712383
;  GENERAL INFORMATION:
;    APPLICANT:  Sheridan, Patrick
;    APPLICANT:  Chang, Chu-An
;    APPLICANT:  Running, Joyce
;    APPLICANT:  Urdea, Michael S.
;    TITLE OF INVENTION:  PROCESS FOR IMMOBILIZING NUCLEIC ACID
;    TITLE OF INVENTION:  PROBES ON POLYSTYRENE SURFACES
;    NUMBER OF SEQUENCES:  70
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CHIRON CORPORATION - R440
;      STREET:  P.O. Box 8097
;      CITY:  Emeryville
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94662-8097
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/438,639
;      FILING DATE:  10-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/813,338
;      FILING DATE:  23-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Goldman, Kenneth, M.
;      REGISTRATION NUMBER:  34,174
;      REFERENCE/DOCKET NUMBER:  0232.001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 601-2719
;      TELEFAX:  (510) 655-3542
;      TELEX:  N/A
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  33 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-438-639-15


  Query Match             84.6%;  Score 11;  DB 1;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 caagaaagaca 11
          ||||||||||||
Db      9 CAAGAAAGACA 19


RESULT   8
US-07-813-338A-15
; Sequence 15, Application US/07813338A
; Patent No. 5747244
;  GENERAL INFORMATION:
;    APPLICANT:  Sheridan, Patrick
;    APPLICANT:  Chang, Chu-An
;    APPLICANT:  Running, Joyce
;    APPLICANT:  Urdea, Michael S.
;    TITLE OF INVENTION:  PROCESS FOR IMMOBILIZING NUCLEIC ACID
;    TITLE OF INVENTION:  PROBES ON POLYSTYRENE SURFACES
;    NUMBER OF SEQUENCES:  70
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CHIRON CORPORATION - R440
;      STREET:  P.O. Box 8097
;      CITY:  Emeryville
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94662-8097
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/813,338A
;      FILING DATE:  23-DEC-1991
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Goldman, Kenneth, M.
;      REGISTRATION NUMBER:  34,174
;      REFERENCE/DOCKET NUMBER:  0232.001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 601-2719
;      TELEFAX:  (510) 655-3542
;      TELEX:  N/A
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  33 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-07-813-338A-15


  Query Match             84.6%;  Score 11;  DB 1;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 caagaaagaca 11
          ||||||||||||
Db      9 CAAGAAAGACA 19


RESULT   9
US-08-441-971-90
; Sequence 90, Application US/08441971
; Patent No. 6071693
;  GENERAL INFORMATION:
;    APPLICANT:  Tai-An Cha
;    TITLE OF INVENTION:  HCV GENOMIC SEQUENCES FOR
;    TITLE OF INVENTION:  DIAGNOSTICS AND THERAPEUTICS
;    NUMBER OF SEQUENCES:  147
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  MS-DOS Version 3.3
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/441,971
;      FILING DATE:  16-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
```

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 23, 2001, 16:04:31 ; Search time 551.33 Seconds
(without alignments)
11.583 Million cell updates/sec

Title: US-09-554-267-3
Perfect score: 17
Sequence: 1 ggcccccatggtggagg 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 624296

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_36:*
1: /cgn2_2/gcgdata/geneseq/geneseqn/NA1980.DAT:*
2: /cgn2_2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
3: /cgn2_2/gcgdata/geneseq/geneseqn/NA1982.DAT:*
4: /cgn2_2/gcgdata/geneseq/geneseqn/NA1983.DAT:*
5: /cgn2_2/gcgdata/geneseq/geneseqn/NA1984.DAT:*
6: /cgn2_2/gcgdata/geneseq/geneseqn/NA1985.DAT:*
7: /cgn2_2/gcgdata/geneseq/geneseqn/NA1986.DAT:*
8: /cgn2_2/gcgdata/geneseq/geneseqn/NA1987.DAT:*
9: /cgn2_2/gcgdata/geneseq/geneseqn/NA1988.DAT:*
10: /cgn2_2/gcgdata/geneseq/geneseqn/NA1989.DAT:*
11: /cgn2_2/gcgdata/geneseq/geneseqn/NA1990.DAT:*
12: /cgn2_2/gcgdata/geneseq/geneseqn/NA1991.DAT:*
13: /cgn2_2/gcgdata/geneseq/geneseqn/NA1992.DAT:*
14: /cgn2_2/gcgdata/geneseq/geneseqn/NA1993.DAT:*
15: /cgn2_2/gcgdata/geneseq/geneseqn/NA1994.DAT:*
16: /cgn2_2/gcgdata/geneseq/geneseqn/NA1995.DAT:*
17: /cgn2_2/gcgdata/geneseq/geneseqn/NA1996.DAT:*
18: /cgn2_2/gcgdata/geneseq/geneseqn/NA1997.DAT:*
19: /cgn2_2/gcgdata/geneseq/geneseqn/NA1998.DAT:*
20: /cgn2_2/gcgdata/geneseq/geneseqn/NA1999.DAT:*
21: /cgn2_2/gcgdata/geneseq/geneseqn/NA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	17	100.0	18	15	Q77634	Ribonucleotide to
c	2	17	100.0	18	15	Q77620	Antisense polynucl
c	3	17	100.0	18	15	Q77648	Antisense ribonucl
	4	17	100.0	18	15	Q76393	Polynucleotide to
c	5	17	100.0	36	15	Q76387	Tenascin gene cons
	6	17	100.0	36	15	Q76386	Tenascin gene cons
c	7	17	100.0	36	15	Q77661	Tenascin gene mRNA
	8	17	100.0	36	15	Q77662	Tenascin gene mRNA
	9	15	88.2	24	15	Q77617	Polynucleotide to
c	10	15	88.2	24	15	Q77659	Antisense ribonucl
c	11	15	88.2	24	15	Q77631	Antisense polynucl
	12	15	88.2	24	15	Q77645	Ribonucleotide to
	13	14.4	84.7	34	19	V68229	Human cytostatin I
c	14	14.4	84.7	35	20	Z33020	Human ATR-5 L chai
c	15	14	82.4	34	17	T10560	Serum paraoxonase
c	16	13.8	81.2	31	21	Z58151	Human FAST-1 gene
c	17	13.8	81.2	41	18	T97210	Kappa chain variab
c	18	13.4	78.8	24	21	Z61427	PCR primer for DNA
c	19	13.4	78.8	27	18	T90893	5' primer for epid
	20	13.4	78.8	27	20	X88424	IBV M protein PCR
c	21	13.4	78.8	31	18	T68725	Human osteo antivi
c	22	13.4	78.8	31	19	V45332	Human extracellula
c	23	13.4	78.8	32	17	T39712	Ubiquitin conjugat
c	24	13.4	78.8	32	18	T79829	Primer used for am
c	25	13.4	78.8	32	20	Z25321	Human ubiquitin co
c	26	13.4	78.8	32	20	V82882	5' PCR primer used
c	27	13.4	78.8	33	17	T39706	Ubiquitin conjugat
c	28	13.4	78.8	33	18	T79823	Primer used for am
c	29	13.4	78.8	33	20	Z25315	Human ubiquitin co
c	30	13.4	78.8	33	20	V82876	5' PCR primer used
c	31	13.4	78.8	35	20	X36573	PCR primer for hum
c	32	13.4	78.8	43	17	T42077	Human erythropoiet
c	33	13.4	78.8	47	15	Q68640	A33 heavy chain va
c	34	13.4	78.8	47	16	Q80383	Mouse light chain
c	35	13.4	78.8	47	16	Q80450	L243 VL region 5'
c	36	13	76.5	24	16	Q80830	Lipopolysaccharide
c	37	13	76.5	24	19	V10334	Human rLBP PCR pri
c	38	12.8	75.3	18	15	Q55636	Juniperus Cry j I
c	39	12.8	75.3	27	19	V19570	Human LDL receptor
c	40	12.8	75.3	30	20	X81805	PCR primer used to
c	41	12.8	75.3	33	21	Z38653	H2O-Th fusion gene
c	42	12.8	75.3	35	17	T32397	PCR primer for nef
c	43	12.8	75.3	35	19	V85960	Human LRP-3 cDNA P
c	44	12.8	75.3	36	11	Q06526	36 mer probe used
	45	12.8	75.3	36	19	T97442	Human cytokine rec

ALIGNMENTS

RESULT 1
Q77634
ID Q77634 standard; RNA; 18 BP.
XX
AC Q77634;
XX
DT 02-JUN-1995 (first entry)
XX
DE Ribonucleotide to tenascin gene consensus mRNA initiation site -9-+9.
XX
KW Antisense; polynucleotide; sense strand; tenascin; complementary;
KW consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW proliferation; growth stimulatory; transcription; vascular stenosis;
KW post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW organ transplant; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_difference 1..18
FT /*tag= a
FT /note= "phosphodiester bonds between nucleotides
FT may be replaced by phosphorothioate bonds"
FT
XX
PN WO9421664-A
XX
PD 29-SEP-1994.
XX
PF 24-MAR-1994; 94WO-US03206.
XX
PR 25-MAR-1993; 93US-0037025.
XX
PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI Denner LA, Dixon RAF, Rege AA, Stacy DL;

```
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 5; Page 47; 64pp; English.
XX
CC   A series of polynucleotides, either DNA (Q76388 and Q76392-400 and
CC   Q77614-18) or RNA (Q76390 and Q77633-46), directed against the consensus
CC   mRNA initiation site sequence (Q77661) for the tenascin gene.  The
CC   polynucleotides are based on the degenerate sequence (Q76386) of the
CC   tenascin gene.  Tenascin is an extracellular matrix glycoprotein
CC   consisting six disulphide-linked subunits, each having molecular mass of
CC   190-250 kDa.  Tenascin may be important for smooth muscle cell
CC   proliferation as the protein has growth stimulatory activity.  The
CC   polynucleotides can be used to inhibit transcription of the gene or
CC   translation of the mRNA encoding tenascin. The method is applicable to a
CC   number of diseases where the proliferation of smooth muscle is involved
CC   e.g. vascular stenosis, post-angioplasty restenosis and other
CC   non-angioplasty procedures such as cardiac hypertrophy, vascular surgery
CC   and organ transplant.
XX
SQ   Sequence 18 BP; 2 A; 5 C; 8 G; 3 U; 0 other;

  Query Match             100.0%;  Score 17;  DB 15;  Length 18;
  Best Local Similarity   88.2%;  Pred. No. 7.7;
  Matches   15;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggccccccatggtggagg 17
          ||||||||:||:|||||
Db      1 ggccccccaugguggagg 17


RESULT   2
Q77620/c
ID   Q77620 standard; DNA; 18 BP.
XX
AC   Q77620;
XX
DT   01-JUN-1995  (first entry)
XX
DE   Antisense polynucleotide binds to tenascin gene consensus at -9-+9.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..18
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                          may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 10; Page 44; 64pp; English.
XX
CC   A series of antisense polynucleotides, either DNA (Q76388 and Q77619-32)
CC   or RNA (Q76390 and Q77647-60) directed against the sense strand of the
CC   gene encoding tenascin.  The polynucleotides are based on the
CC   complementary sequence (Q76386) of the consensus mRNA initiation site
CC   sequence (Q77661) for the tenascin gene.  Tenascin is an extracellular
CC   matrix glycoprotein consisting six disulphide-linked subunits, each
CC   having molecular mass of 190-250 kDa.  Tenascin may be important for
CC   smooth muscle cell proliferation as the protein has growth stimulatory
CC   activity.  The polynucleotides can be used to inhibit transcription
CC   of the gene or translation of the mRNA encoding tenascin.  The method is
CC   applicable to a number of diseases where the proliferation of smooth
CC   muscle is involved e.g. vascular stenosis, post-angioplasty restenosis
CC   and other non-angioplasty procedures such as cardiac hypertrophy,
CC   vascular surgery and organ transplant.
XX
SQ   Sequence 18 BP; 3 A; 8 C; 5 G; 2 T; 0 other;

  Query Match             100.0%;  Score 17;  DB 15;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.7;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggccccccatggtggagg 17
          |||||||||||||||||
Db     18 GGCCCCCATGGTGGAGG 2


RESULT   3
Q77648/c
ID   Q77648 standard; RNA; 18 BP.
XX
AC   Q77648;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Antisense ribonucleotide binds to tenascin gene consensus at -9-+9.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..18
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                          may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
```

```
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 10; Page 51; 64pp; English.
XX
CC   A series of antisense polynucleotides, either DNA (Q76388 and Q77619-32)
CC   or RNA (Q76390 and Q77647-60) directed against the sense strand of the
CC   gene encoding tenascin.  The polynucleotides are based on the
CC   complementary sequence (Q76386) of the consensus mRNA initiation site
CC   sequence (Q77661) for the tenascin gene.  Tenascin is an extracellular
CC   matrix glycoprotein consisting six disulphide-linked subunits, each
CC   having molecular mass of 190-250 kDa.  Tenascin may be important for
CC   smooth muscle cell proliferation as the protein has growth stimulatory
CC   activity.  The polynucleotides can be used to inhibit transcription
CC   of the gene or translation of the mRNA encoding tenascin.  The method is
CC   applicable to a number of diseases where the proliferation of smooth
CC   muscle is involved e.g. vascular stenosis, post-angioplasty restenosis
CC   and other non-angioplasty procedures such as cardiac hypertrophy,
CC   vascular surgery and organ transplant.
XX
SQ   Sequence 18 BP; 3 A; 8 C; 5 G; 2 U; 0 other;


  Query Match             100.0%;  Score 17;  DB 15;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.7;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggccccccatggtggagg 17
          |||||||||||||||||
Db     18 GGCCCCCATGGTGGAGG 2


RESULT  4
Q76393
ID   Q76393 standard; DNA; 18 BP.
XX
AC   Q76393;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Polynucleotide to tenascin gene consensus mRNA initiation site -9-+9.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..18
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                           may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 5; Page 40; 64pp; English.
XX
CC   A series of polynucleotides, either DNA (Q76388 and Q76392-400 and
CC   Q77614-18) or RNA (Q76390 and Q77633-46), directed against the consensus
CC   mRNA initiation site sequence (Q77661) for the tenascin gene.  The
CC   polynucleotides are based on the degenerate sequence (Q76386) of the
CC   tenascin gene.  Tenascin is an extracellular matrix glycoprotein
CC   consisting six disulphide-linked subunits, each having molecular mass of
CC   190-250 kDa.  Tenascin may be important for smooth muscle cell
CC   proliferation as the protein has growth stimulatory activity.  The
CC   polynucleotides can be used to inhibit transcription of the gene or
CC   translation of the mRNA encoding tenascin. The method is applicable to a
CC   number of diseases where the proliferation of smooth muscle is involved
CC   e.g. vascular stenosis, post-angioplasty restenosis and other
CC   non-angioplasty procedures such as cardiac hypertrophy, vascular surgery
CC   and organ transplant.
XX
SQ   Sequence 18 BP; 2 A; 5 C; 8 G; 3 T; 0 other;


  Query Match             100.0%;  Score 17;  DB 15;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.7;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggccccccatggtggagg 17
          |||||||||||||||||
Db      1 ggccccccatggtggagg 17


RESULT  5
Q76387/c
ID   Q76387 standard; DNA; 36 BP.
XX
AC   Q76387;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Tenascin gene consensus DNA sequence sense strand.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..36
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                           may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 6; Page 39; 64pp; English.
```

```
XX
CC   A series of polynucleotides, either DNA (Q76389 and Q76392-400 and
CC   Q77614-18) or RNA (Q76391 and Q77633-46), directed against the consensus
CC   mRNA initiation site sequence (Q77661) for the tenascin gene.  The
CC   polynucleotides are based on the sense strand sequence (Q76387) of the
CC   tenascin gene.  Tenascin is an extracellular matrix glycoprotein
CC   consisting six disulphide-linked subunits, each having molecular mass of
CC   190-250 kDa.  Tenascin may be important for smooth muscle cell
CC   proliferation as the protein has growth stimulatory activity.  The
CC   polynucleotides can be used to inhibit transcription of the gene or
CC   translation of the mRNA encoding tenascin. The method is applicable to a
CC   number of diseases where the proliferation of smooth muscle is involved
CC   e.g. vascular stenosis, post-angioplasty restenosis and other
CC   non-angioplasty procedures such as cardiac hypertrophy, vascular surgery
CC   and organ transplant.
XX
SQ   Sequence 36 BP; 5 A; 12 C; 8 G; 5 T; 6 other;


  Query Match             100.0%;  Score 17;  DB 15;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 7.9;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggccccccatggtggagg 17
          |||||||||||||||||
Db     18 GGCCCCCATGGTGGAGG 2


RESULT   6
Q76386
ID   Q76386 standard; DNA; 36 BP.
XX
AC   Q76386;
XX
DT   01-JUN-1995  (first entry)
XX
DE   Tenascin gene consensus DNA sequence antisense strand.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..36
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                          may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 1; Page 38; 64pp; English.
XX
CC   A series of antisense polynucleotides, either DNA (Q76388 and Q77619-32)
CC   or RNA (Q76390 and Q77647-60) directed against the sense strand of the
CC   gene encoding tenascin.  The polynucleotides are based on the
CC   complementary sequence (Q76386) of the consensus mRNA initiation site
CC   sequence (Q77661) for the tenascin gene.  Tenascin is an extracellular
CC   matrix glycoprotein consisting six disulphide-linked subunits, each
CC   having molecular mass of 190-250 kDa.  Tenascin may be important for
CC   smooth muscle cell proliferation as the protein has growth stimulatory
CC   activity.  The polynucleotides can be used to inhibit transcription
CC   of the gene or translation of the mRNA encoding tenascin.  The method is
CC   applicable to a number of diseases where the proliferation of smooth
CC   muscle is involved e.g. vascular stenosis, post-angioplasty restenosis
CC   and other non-angioplasty procedures such as cardiac hypertrophy,
CC   vascular surgery and organ transplant.
XX
SQ   Sequence 36 BP; 5 A; 8 C; 12 G; 5 T; 6 other;


  Query Match             100.0%;  Score 17;  DB 15;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 7.9;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggccccccatggtggagg 17
          |||||||||||||||||
Db     19 ggccccccatggtggagg 35


RESULT   7
Q77661/c
ID   Q77661 standard; RNA; 36 BP.
XX
AC   Q77661;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Tenascin gene mRNA initiation site consensus sequence.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Disclosure; Page 7; 64pp; English.
XX
CC   The  consensus sequence surrounding the initiation site of the mRNA for
CC   the tenascin gene.  The sequence was used to generate the corresponding
CC   DNA sequence (Q77662).  The sequences were the basis for generating a
CC   series of polynucleotides (Q76388-400 and Q77614-60) which were targeted
CC   against either the mRNA or the strand coding for the mRNA of the tenascin
CC   gene.  The polynucleotides can be used to inhibit transcription of the
CC   gene or translation of the mRNA encoding tenascin. Tenascin is an
CC   extracellular matrix glycoprotein consisting six disulphide-linked
CC   subunits, each having molecular mass of 190-250 kDa.  Tenascin may be
```

```
CC   important for smooth muscle cell proliferation as the protein has growth
CC   stimulatory activity.  The method is applicable to a number of diseases
CC   where the proliferation of smooth muscle is involved e.g. vascular
CC   stenosis, post-angioplasty restenosis and other non-angioplasty
CC   procedures such as cardiac hypertrophy, vascular surgery and organ
CC   transplant.
XX
SQ   Sequence 36 BP; 5 A; 12 C; 8 G; 5 U; 6 other;


  Query Match             100.0%;  Score 17;  DB 15;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 7.9;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggccccccatggtggagg 17
          |||||||||||||||||
Db     18 GGCCCCCATGGTGGAGG 2


RESULT   8
Q77662
ID   Q77662 standard; DNA; 36 BP.
XX
AC   Q77662;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Tenascin gene mRNA initiation site complementary DNA sequence.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Disclosure; Page 54; 64pp; English.
XX
CC   The DNA sequence corresponding to the consensus sequence (Q77661)
CC   surrounding the initiation site of the mRNA for the tenascin gene.  The
CC   sequences were the basis for generating a series of polynucleotides
CC   (Q76386-400 and Q77614-60) which were targeted against either the mRNA or
CC   the strand coding for the mRNA of the tenascin gene.  The polynucleotides
CC   can be used to inhibit transcription of the gene or translation of the
CC   mRNA encoding tenascin. Tenascin is an extracellular matrix glycoprotein
CC   consisting six disulphide-linked subunits, each having molecular mass of
CC   190-250 kDa.  Tenascin may be important for smooth muscle cell
CC   proliferation as the protein has growth stimulatory activity.  The method
CC   is applicable to a number of diseases where the proliferation of smooth
CC   muscle is involved e.g. vascular stenosis, post-angioplasty restenosis
CC   and other non-angioplasty procedures such as cardiac hypertrophy,
CC   vascular surgery and organ transplant.
XX
SQ   Sequence 36 BP; 5 A; 8 C; 12 G; 5 T; 6 other;


  Query Match             100.0%;  Score 17;  DB 15;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 7.9;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggccccccatggtggagg 17
          |||||||||||||||||
Db     19 ggccccccatggtggagg 35


RESULT   9
Q77617
ID   Q77617 standard; DNA; 24 BP.
XX
AC   Q77617;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Polynucleotide to tenascin gene consensus mRNA initiation site -6-+18.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..24
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                          may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 5; Page 43; 64pp; English.
XX
CC   A series of polynucleotides, either DNA (Q76388 and Q76392-400 and
CC   Q77614-18) or RNA (Q76390 and Q77633-46), directed against the consensus
CC   mRNA initiation site sequence (Q77661) for the tenascin gene.  The
CC   polynucleotides are based on the degenerate sequence (Q76386) of the
CC   tenascin gene.  Tenascin is an extracellular matrix glycoprotein
CC   consisting six disulphide-linked subunits, each having molecular mass of
CC   190-250 kDa.  Tenascin may be important for smooth muscle cell
CC   proliferation as the protein has growth stimulatory activity.  The
CC   polynucleotides can be used to inhibit transcription of the gene or
CC   translation of the mRNA encoding tenascin. The method is applicable to a
CC   number of diseases where the proliferation of smooth muscle is involved
CC   e.g. vascular stenosis, post-angioplasty restenosis and other
CC   non-angioplasty procedures such as cardiac hypertrophy, vascular surgery
CC   and organ transplant.
XX
SQ   Sequence 24 BP; 4 A; 7 C; 8 G; 5 T; 0 other;
```

```
  Query Match             88.2%;  Score 15;  DB 15;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggcccccatggtgga 15
          |||||||||||||||
Db     10 ggcccccatggtgga 24


RESULT  10
Q77659/c
ID   Q77659 standard; RNA; 24 BP.
XX
AC   Q77659;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Antisense ribonucleotide binds to tenascin gene consensus at -6-+18.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..24
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                          may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 10; Page 53; 64pp; English.
XX
CC   A series of antisense polynucleotides, either DNA (Q76388 and Q77619-32)
CC   or RNA (Q76390 and Q77647-60) directed against the sense strand of the
CC   gene encoding tenascin.  The polynucleotides are based on the
CC   complementary sequence (Q76386) of the consensus mRNA initiation site
CC   sequence (Q77661) for the tenascin gene.  Tenascin is an extracellular
CC   matrix glycoprotein consisting six disulphide-linked subunits, each
CC   having molecular mass of 190-250 kDa.  Tenascin may be important for
CC   smooth muscle cell proliferation as the protein has growth stimulatory
CC   activity.  The polynucleotides can be used to inhibit transcription
CC   of the gene or translation of the mRNA encoding tenascin.  The method is
CC   applicable to a number of diseases where the proliferation of smooth
CC   muscle is involved e.g. vascular stenosis, post-angioplasty restenosis
CC   and other non-angioplasty procedures such as cardiac hypertrophy,
CC   vascular surgery and organ transplant.
XX
SQ   Sequence 24 BP; 5 A; 8 C; 7 G; 4 U; 0 other;

  Query Match             88.2%;  Score 15;  DB 15;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggcccccatggtgga 15
          |||||||||||||||
Db     15 GGCCCCCATGGTGGA 1


RESULT  11
Q77631/c
ID   Q77631 standard; DNA; 24 BP.
XX
AC   Q77631;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Antisense polynucleotide binds to tenascin gene consensus at -6-+18.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..24
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                          may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 10; Page 46; 64pp; English.
XX
CC   A series of antisense polynucleotides, either DNA (Q76388 and Q77619-32)
CC   or RNA (Q76390 and Q77647-60) directed against the sense strand of the
CC   gene encoding tenascin.  The polynucleotides are based on the
CC   complementary sequence (Q76386) of the consensus mRNA initiation site
CC   sequence (Q77661) for the tenascin gene.  Tenascin is an extracellular
CC   matrix glycoprotein consisting six disulphide-linked subunits, each
CC   having molecular mass of 190-250 kDa.  Tenascin may be important for
CC   smooth muscle cell proliferation as the protein has growth stimulatory
CC   activity.  The polynucleotides can be used to inhibit transcription
CC   of the gene or translation of the mRNA encoding tenascin.  The method is
CC   applicable to a number of diseases where the proliferation of smooth
CC   muscle is involved e.g. vascular stenosis, post-angioplasty restenosis
CC   and other non-angioplasty procedures such as cardiac hypertrophy,
CC   vascular surgery and organ transplant.
XX
SQ   Sequence 24 BP; 5 A; 8 C; 7 G; 4 T; 0 other;

  Query Match             88.2%;  Score 15;  DB 15;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy      1 ggccccccatggtgga 15
          ||||||||||||||||
Db     15 GGCCCCCCATGGTGGA 1
```

```
RESULT  12
Q77645
ID   Q77645 standard; RNA; 24 BP.
XX
AC   Q77645;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Ribonucleotide to tenascin gene consensus mRNA initiation site -6-+18.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..24
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                          may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 5; Page 50; 64pp; English.
XX
CC   A series of polynucleotides, either DNA (Q76388 and Q76392-400 and
CC   Q77614-18) or RNA (Q76390 and Q77633-46), directed against the consensus
CC   mRNA initiation site sequence (Q77661) for the tenascin gene.  The
CC   polynucleotides are based on the degenerate sequence (Q76386) of the
CC   tenascin gene.  Tenascin is an extracellular matrix glycoprotein
CC   consisting six disulphide-linked subunits, each having molecular mass of
CC   190-250 kDa.  Tenascin may be important for smooth muscle cell
CC   proliferation as the protein has growth stimulatory activity.  The
CC   polynucleotides can be used to inhibit transcription of the gene or
CC   translation of the mRNA encoding tenascin. The method is applicable to a
CC   number of diseases where the proliferation of smooth muscle is involved
CC   e.g. vascular stenosis, post-angioplasty restenosis and other
CC   non-angioplasty procedures such as cardiac hypertrophy, vascular surgery
CC   and organ transplant.
XX
SQ   Sequence 24 BP; 4 A; 7 C; 8 G; 5 U; 0 other;
```

```
  Query Match           88.2%;  Score 15;  DB 15;  Length 24;
  Best Local Similarity  86.7%;  Pred. No. 73;
  Matches   13;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggccccccatggtgga 15
          ||||||||:||:|||
Db     10 ggcccccauggugga 24
```

```
RESULT  13
V68229
ID   V68229 standard; DNA; 34 BP.
XX
AC   V68229;
XX
DT   29-JAN-1999  (first entry)
XX
DE   Human cytostatin II primer 4.
XX
KW   ss; human; PCR; primer; amplification; cytostatin; cell growth;
KW   tumour; nervous system; viral infection; microbial infection.
XX
OS   Homo sapiens.
XX
PN   WO9844109-A1.
XX
PD   08-OCT-1998.
XX
PF   25-MAR-1998;   98WO-US05839.
XX
PR   27-MAR-1997;   97US-0041645.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (LONG-) LONG ISLAND JEWISH MEDICAL CENT.
XX
PI   Gentz RL,  Nardelli B,  Ni J,  Shi YE,  Yu G;
XX
DR   WPI; 1998-557110/47.
XX
PT   New isolated human cytostatin II - used to develop products for the
PT   treatment of e.g. cancers or viral or microbial infections or for
PT   protecting nervous system cells from toxic agents
XX
PS   Example 3; Page 49; 73pp; English.
XX
CC   The primers V68226-V68231 were used in the expression of Human
CC   cytostatin, which inhibits cell growth and modulates differentiation.
CC   The cytostatin II polypeptides can be used for inhibiting tumour growth
CC   in a subject, for stimulating growth of or protecting nervous system
CC   cells from toxic agents or for protecting against or treating viral or
CC   microbial infections in mammals.  The products can also be used e.g. to
CC   modulate angiogenesis, to modulate breast development and milk
CC   production.  They can also be used in cerebella granular cells and photo
CC   receptor cells to provide protection from lipid peroxidation associated
CC   with the oxidative stress induced during early stages of ischemia,
CC   apoptosis, and excitatory amino acid induced cell death.  The retinoid
CC   binding potential of cytostatin II may be used on photo receptor cells in
CC   vivo or in vitro.  The activity of haematopoiesis indicates a possible
CC   immunosuppressive activity or a lineage specific stimulation of
CC   haematopoiesis which could be used for treating conditions requiring
CC   immunosuppression.  Antagonists to cytostatin II may be used in vivo to
CC   induce deficiencies or enhancement in the immune or in the haematopoietic
CC   systems.  They may be used e.g. to treat cardiac myocyte hypertrophy or
CC   leukemia.
XX
SQ   Sequence 34 BP; 4 A; 10 C; 12 G; 8 T; 0 other;
```

```
  Query Match           84.7%;  Score 14.4;  DB 19;  Length 34;
  Best Local Similarity  93.8%;  Pred. No. 1.5e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 gcccccatggtggagg 17
          ||| ||||||||||||
Db     11 gccaccatggtggagg 26
```

```
RESULT  14
Z33020/c
```

ID Z33020 standard; DNA; 35 BP.
XX
AC Z33020;
XX
DT 26-JAN-2000 (first entry)
XX
DE Human ATR-5 L chain V region PCR primer ch5LS.
XX
KW Human tissue factor; TF; humanised; antibody; mouse monoclonal antibody;
KW ATR-2; ATR-3; ATR-4; ATR-5; ATR-7; ATR-8; thrombotic disease; DIC;
KW disseminated intravascular coagulation; immunogenicity; chimeric; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9951743-A1.
XX
PD 14-OCT-1999.
XX
PF 02-APR-1999; 99WO-JP01768.
XX
PR 03-APR-1998; 98JP-0091850.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
XX
PI Sato K, Adachi H, Yabuta N;
XX
DR WPI; 1999-620204/53.
XX
PT Humanised antibody recognizing human tissue factor, used for treatment
PT of disseminated intravascular coagulation
XX
PS Example 2; Page 199; 291pp; Japanese.
XX
CC The present invention describes chimeric antibody (Ab) heavy (H) chains
CC containing the variable region of the H chain of a mouse monoclonal Ab
CC recognising human tissue factor (hTF) and the constant region of the H
CC chain of a human Ab. The variable region is one of six specified
CC sequences (which are the H chain variable regions from mouse monoclonal
CC Ab's ATR-2,3,4,5,7 or 8). Also described are chimeric Ab light (L) chains
CC containing the variable region of the L chain of a mouse monoclonal Ab
CC recognising human tissue factor (hTF) and the constant region of the L
CC chain of a human Ab, the variable region being one of six specified
CC sequences (which are the L chain variable regions from mouse monoclonal
CC Ab's ATR-2,3,4,5,7 or 8). The chimeric Ab's can be used for the treatment
CC and prevention of thrombotic disease, especially of disseminated
CC intravascular coagulation (DIC). The humanised antibody has the high hTF
CC binding activity of the mouse monoclonal antibody but greatly reduced
CC immunogenicity. Z33001 to Z33091 and Y527007 to Y52767 represent
CC sequences used in the exemplification of the present invention.
XX
SQ Sequence 35 BP; 6 A; 12 C; 8 G; 9 T; 0 other;

Query Match 84.7%; Score 14.4; DB 20; Length 35;
Best Local Similarity 93.8%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ggcccccatggtggag 16
|||||.||||||||||
Db 24 GGCCCTCATGGTGGAG 9

RESULT 15
T10560/c
ID T10560 standard; DNA; 34 BP.
XX
AC T10560;
XX
DT 21-JUL-1996 (first entry)
XX
DE Serum paraoxonase 5' PCR primer.
XX
KW Paraoxonase; SPP; neurotoxin; anticholinesterase; organophosphate;
KW antidote; gene therapy; polymerase chain reaction; primer; PCR; ss.
XX
OS Synthetic.
XX
PN WO9601322-A1.
XX
PD 18-JAN-1996.
XX
PF 28-JUN-1995; 95WO-US08111.
XX
PR 05-JUL-1994; 94US-0270583.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI He WW, Hudson PL, Ruben SM;
XX
DR WPI; 1996-087672/09.
XX
PT Polynucleotide encoding human serum paraoxonase polypeptide (SPP)
PT used as antidote to neurotoxic organo:phosphate(s), for diagnosing
PT SPP underexpression related diseases and for identifying SPP
PT agonists.
XX
PS Example 1; Page 30; 50pp; English.
XX
CC A PCR primer (T10560) contains a BamHI site followed by 21
CC nucleotides of the human serum paraoxonase coding sequence (see
CC also T10557) starting from the initiation codon. It was used with
CC a 3' primer (T10561) for the PCR amplification of paraoxonase
CC DNA. The resulting DNA fragment was fused to a haemagglutinin tag
CC sequence and cloned into the polylinker region of vector pcDNAI/Amp
CC for expression of recombinant paraoxonase in CHO cells. The
CC paraoxonase (see also R88210) is useful as a neurotoxin antidote.
XX
SQ Sequence 34 BP; 3 A; 10 C; 15 G; 6 T; 0 other;

Query Match 82.4%; Score 14; DB 17; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 gcccccatggtgga 15
||||||||||||||
Db 21 GCCCCCATGGTGGA 8

Search completed: March 23, 2001, 16:04:32
Job time: 35931 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 23, 2001, 15:55:07 ; Search time 319.44 Seconds
(without alignments)
8.577 Million cell updates/sec

Title: US-09-554-267-3
Perfect score: 17
Sequence: 1 ggccccccatggtggagg 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 280836 seqs, 80580151 residues

Total number of hits satisfying chosen parameters: 402106

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	15	88.2	21	2	US-08-876-991-8	Sequence 8, Appli
c	2	15	88.2	21	2	US-09-059-853-8	Sequence 8, Appli
	3	14	82.4	30	3	US-08-557-210A-25	Sequence 25, Appl
c	4	14	82.4	34	3	US-09-067-089-5	Sequence 5, Appli
c	5	13.8	81.2	31	3	US-09-113-309-11	Sequence 11, Appl
c	6	13.8	81.2	41	2	US-08-761-277A-67	Sequence 67, Appl
	7	13.4	78.8	27	2	US-08-407-900B-2	Sequence 2, Appli
c	8	13.4	78.8	32	1	US-08-464-342-21	Sequence 21, Appl
c	9	13.4	78.8	32	2	US-08-464-604A-24	Sequence 24, Appl
c	10	13.4	78.8	32	2	US-08-875-272-21	Sequence 21, Appl
c	11	13.4	78.8	32	2	US-08-903-396-21	Sequence 21, Appl
c	12	13.4	78.8	33	1	US-08-464-342-15	Sequence 15, Appl
c	13	13.4	78.8	33	2	US-08-464-604A-18	Sequence 18, Appl
c	14	13.4	78.8	33	2	US-08-875-272-15	Sequence 15, Appl
c	15	13.4	78.8	33	2	US-08-903-396-15	Sequence 15, Appl
c	16	13	76.5	24	1	US-08-261-660A-7	Sequence 7, Appli
c	17	13	76.5	24	4	PCT-US94-06931-7	Sequence 7, Appli
c	18	12.8	75.3	41	2	US-08-761-277A-56	Sequence 56, Appl
c	19	12.4	72.9	24	2	US-08-785-750-11	Sequence 11, Appl
c	20	12.4	72.9	25	2	US-08-467-265-12	Sequence 12, Appl
c	21	12.4	72.9	26	1	US-08-388-779A-11	Sequence 11, Appl
c	22	12.4	72.9	26	1	US-08-591-070A-11	Sequence 11, Appl
c	23	12.4	72.9	26	2	US-08-927-855-11	Sequence 11, Appl
c	24	12.4	72.9	32	3	US-08-889-502-12	Sequence 12, Appl
	25	12.4	72.9	37	4	PCT-US93-11638-6	Sequence 6, Appli
	26	12.4	72.9	45	2	US-08-484-993B-51	Sequence 51, Appl
	27	12.4	72.9	45	2	US-08-484-158B-51	Sequence 51, Appl
	28	12.4	72.9	45	2	US-08-484-596A-51	Sequence 51, Appl
	29	12.4	72.9	45	2	US-08-480-150A-51	Sequence 51, Appl
	30	12.4	72.9	45	3	US-08-458-731-51	Sequence 51, Appl
	31	12.4	72.9	45	3	US-08-149-223A-51	Sequence 51, Appl
c	32	12.2	71.8	21	2	US-08-665-202-131	Sequence 131, App
c	33	12.2	71.8	25	1	US-08-253-575-8	Sequence 8, Appli
	34	12.2	71.8	26	3	US-09-108-020-29	Sequence 29, Appl
c	35	12.2	71.8	32	1	US-08-465-687A-7	Sequence 7, Appli
c	36	12.2	71.8	32	2	US-08-815-718-4	Sequence 4, Appli
c	37	12.2	71.8	32	3	US-08-468-846-5	Sequence 5, Appli
c	38	12.2	71.8	32	3	US-09-030-970-7	Sequence 7, Appli
c	39	12.2	71.8	36	1	US-08-137-117D-46	Sequence 46, Appl
c	40	12.2	71.8	36	1	US-08-436-717-46	Sequence 46, Appl
c	41	12.2	71.8	38	2	US-08-460-529B-7	Sequence 7, Appli
c	42	12.2	71.8	41	2	US-08-761-277A-69	Sequence 69, Appl
c	43	12.2	71.8	42	2	US-08-761-277A-65	Sequence 65, Appl
c	44	12.2	71.8	44	1	US-08-253-877C-45	Sequence 45, Appl
c	45	12.2	71.8	44	2	US-08-452-164A-45	Sequence 45, Appl

ALIGNMENTS

```
RESULT 1
US-08-876-991-8/c
; Sequence 8, Application US/08876991
; Patent No. 5925360
;  GENERAL INFORMATION:
;    APPLICANT:  Gregor Meyers, Tillmann R menapf,
;    APPLICANT:  Heinz-J rgen Thiel
;    TITLE OF INVENTION:  Hog cholera virus vaccine and diagnostic
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Organon Teknika Corporation
;      ADDRESSEE:  Biotechnology Research Institute
;      STREET:  1330-A Piccard Drive
;      CITY:  Rockville
;      STATE:  Maryland
;      COUNTRY:  U.S.A.
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/876,991
;      FILING DATE:  16-JUN-1997
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/747,577
;      FILING DATE:
;      APPLICATION NUMBER:  US/08/650,584
;      FILING DATE:
;      APPLICATION NUMBER:  US/08/469,702
;      FILING DATE:
;      APPLICATION NUMBER:  US/08/123,596
;      FILING DATE:
;      APPLICATION NUMBER:  07/797,554
;      FILING DATE:  22-NOV-1991
;      APPLICATION NUMBER:  US 07/494,991
;      FILING DATE:  16-MAR-1990
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  William M. Blackstone
;      REGISTRATION NUMBER:  29,772
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 258-5200
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
```

```
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  1..21
;      OTHER INFORMATION:  /label= Adaptor_4
;      OTHER INFORMATION:  /note= "Upper strand of Bgl II - BamH I adaptor"
US-08-876-991-8


  Query Match             88.2%;  Score 15;  DB 2;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 64;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggccccccatggtgga 15
          ||||||||||||||||
Db     17 GGCCCCCATGGTGGA 3


RESULT   2
US-09-059-853-8/c
; Sequence 8, Application US/09059853
; Patent No. 5935582
;  GENERAL INFORMATION:
;    APPLICANT:  Gregor Meyers, Tillmann R menapf,
;    APPLICANT:  Heinz-J rgen Thiel
;    TITLE OF INVENTION:  Hog cholera virus vaccine and diagnostic
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Organon Teknika Corporation
;      ADDRESSEE:  Biotechnology Research Institute
;      STREET:  1330-A Piccard Drive
;      CITY:  Rockville
;      STATE:  Maryland
;      COUNTRY:  U.S.A.
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/059,853
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/797,554
;      FILING DATE:  22-NOV-1991
;      APPLICATION NUMBER:  US 07/494,991
;      FILING DATE:  16-MAR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  William M. Blackstone
;      REGISTRATION NUMBER:  29,772
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 258-5200
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  1..21
;      OTHER INFORMATION:  /label= Adaptor_4
;      OTHER INFORMATION:  /note= "Upper strand of Bgl II - BamH I adaptor"
US-09-059-853-8


  Query Match             88.2%;  Score 15;  DB 2;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 64;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggccccccatggtgga 15
          ||||||||||||||||
Db     17 GGCCCCCATGGTGGA 3


RESULT   3
US-08-557-210A-25
; Sequence 25, Application US/08557210A
; Patent No. 6114146
;  GENERAL INFORMATION:
;    APPLICANT:  Herlitschka, Sabine
;    APPLICANT:  Schlokat, Uwe
;    APPLICANT:  Falkner, Falko Guenther
;    APPLICANT:  Dorner, Friedrich
;    TITLE OF INVENTION:  An expression plasmid, a fusion protein, a
;    TITLE OF INVENTION:  transfected eukaryotic cell line, a method of producing for
;    TITLE OF INVENTION:  proteins, a foreign protein preparation as well as a pharma
;    TITLE OF INVENTION:  composition
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/557,210A
;      FILING DATE:  14-NOV-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  A 2099/94
;      FILING DATE:  14-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ISACSON, John P.
;      REGISTRATION NUMBER:  33,715
;      REFERENCE/DOCKET NUMBER:  040433/0142/SOPA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  30 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-557-210A-25


  Query Match             82.4%;  Score 14;  DB 3;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 ccccatggtggagg 17
          ||||||||||||||
Db     10 CCCCATGGTGGAGG 23


RESULT   4
US-09-067-089-5/c
; Sequence 5, Application US/09067089A
; Patent No. 6140093
; GENERAL INFORMATION:
;  APPLICANT: Hudson, Peter L.
;  APPLICANT: He, Wei W.
;  APPLICANT: Ruben, Steven M.
```

```
;  TITLE OF INVENTION: Serum Paraoxnase
;  FILE REFERENCE: PF124D2
;  CURRENT APPLICATION NUMBER: US/09/067,089A
;  CURRENT FILING DATE: 1998-04-27
;  EARLIER APPLICATION NUMBER: 08/783,889
;  EARLIER FILING DATE: 1997-01-16
;  EARLIER APPLICATION NUMBER: 08/270,583
;  EARLIER FILING DATE: 1994-07-05
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 34
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-067-089-5


  Query Match             82.4%;  Score 14;  DB 3;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 gccccccatggtgga 15
          ||||||||||||||
Db     21 GCCCCCATGGTGGA 8


RESULT   5
US-09-113-309-11/c
; Sequence 11, Application US/09113309A
; Patent No. 6110738
; GENERAL INFORMATION:
;  APPLICANT: Zhou, Shibin
;  APPLICANT: Zawel, Leigh
;  APPLICANT: Vogelstein, Bert
;  APPLICANT: Kinzler, Kenneth
;  TITLE OF INVENTION: Human Fast-1 Gene
;  FILE REFERENCE: 01107.10898
;  CURRENT APPLICATION NUMBER: US/09/113,309A
;  CURRENT FILING DATE: 1998-07-10
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
;   LENGTH: 31
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-113-309-11


  Query Match             81.2%;  Score 13.8;  DB 3;  Length 31;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 ggccccccatggtggagg 17
          || ||||||||||| ||
Db     24 GGGCCCCATGGTGGCGG 8


RESULT   6
US-08-761-277A-67/c
; Sequence 67, Application US/08761277A
; Patent No. 5972334
;  GENERAL INFORMATION:
;    APPLICANT:  Denney Jr., Dan W.
;    TITLE OF INVENTION:  Vaccines For Treatment Of Lymphoma And
;    TITLE OF INVENTION:  Leukemia
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/761,277A
;      FILING DATE:  06-DEC-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/644,664
;      FILING DATE:  01-MAY-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MacKnight, Kamrin T.
;      REGISTRATION NUMBER:  38,230
;      REFERENCE/DOCKET NUMBER:  GENITOPE-02406
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  67:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  41 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-761-277A-67


  Query Match             81.2%;  Score 13.8;  DB 2;  Length 41;
  Best Local Similarity   88.2%;  Pred. No. 2.3e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 ggccccccatggtggagg 17
          || ||||||||||| |
Db     30 GGACCCCATGGTGGACG 14


RESULT   7
US-08-407-900B-2
; Sequence 2, Application US/08407900B
; Patent No. 5935822
;  GENERAL INFORMATION:
;    APPLICANT:  Staehlin, Andrew
;    APPLICANT:  Galbraith, David
;    APPLICANT:  Giddings, Thomas
;    TITLE OF INVENTION:  PRODUCT AND PROCESS FOR MEMBRANE AND
;    TITLE OF INVENTION:  SOLUBLE POLYPEPTIDE SEGREGATION
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sheridan Ross P.C.
;      STREET:  1700 Lincoln Street, Suite 3500
;      CITY:  Denver
;      STATE:  CO
;      COUNTRY:  U.S.A.
;      ZIP:  80203
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/407,900B
;      FILING DATE:  03-MAR-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kovarik, Joseph E.
;      REGISTRATION NUMBER:  33,005
;      REFERENCE/DOCKET NUMBER:  2848-12
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  303/863-9700
;      TELEFAX:  303/863-0223
;  INFORMATION FOR SEQ ID NO:  2:
```

```
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..27
;      OTHER INFORMATION:  /label= primer
US-08-407-900B-2


  Query Match             78.8%;  Score 13.4;  DB 2;  Length 27;
  Best Local Similarity   93.3%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 ggccccccatggtgga 15
          ||||||||||||| |
Db      1 GGCCCCCATGGTGTA 15


RESULT   8
US-08-464-342-21/c
; Sequence 21, Application US/08464342
; Patent No. 5650313
;  GENERAL INFORMATION:
;    APPLICANT:  NI, ET AL.
;    TITLE OF INVENTION:  Ubiquitin Conjugating Enzymes
;    TITLE OF INVENTION:  7, 8 and 9
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/464,342
;      FILING DATE:  5 JUN 95
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/01250
;      FILING DATE:  31 JAN 95
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MULLINS, J.G.
;      REGISTRATION NUMBER:  33,073
;      REFERENCE/DOCKET NUMBER:  325800-373
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  32 BASE PAIRS
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  SINGLE
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  Oligonucleotide
US-08-464-342-21


  Query Match             78.8%;  Score 13.4;  DB 1;  Length 32;
  Best Local Similarity   93.3%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 ggccccccatggtgga 15
```

```
          |||| ||||||||||
Db     22 GGCCGCCATGGTGGA 8


RESULT   9
US-08-464-604A-24/c
; Sequence 24, Application US/08464604A
; Patent No. 5849286
;  GENERAL INFORMATION:
;    APPLICANT:  NI, JIAN
;    APPLICANT:  GENTZ, REINER
;    APPLICANT:  ADAMS, MARK D
;    TITLE OF INVENTION:  UBIQUITIN CONJUGATING ENZYMES 7, 8 AND 9
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
;      ADDRESSEE:  STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/464,604A
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FERRARO, GREGORY D
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-419
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  32 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-464-604A-24


  Query Match             78.8%;  Score 13.4;  DB 2;  Length 32;
  Best Local Similarity   93.3%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 ggccccccatggtgga 15
          |||| ||||||||||
Db     22 GGCCGCCATGGTGGA 8


RESULT  10
US-08-875-272-21/c
; Sequence 21, Application US/08875272
; Patent No. 5945321
;  GENERAL INFORMATION:
;    APPLICANT:  NI, ET AL.
;    TITLE OF INVENTION:  Ubiquitin Conjugating Enzymes 7, 8 and 9
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
```

```
;       MEDIUM TYPE:  3.5 INCH DISKETTE
;       COMPUTER:  IBM PS/2
;       OPERATING SYSTEM:  MS-DOS
;       SOFTWARE:  WORD PERFECT 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/875,272
;       FILING DATE:  Concurrently
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  FERRARO, GREGORY D.
;       REGISTRATION NUMBER:  36,134
;       REFERENCE/DOCKET NUMBER:  325800-244
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  201-994-1700
;       TELEFAX:  201-994-1744
;   INFORMATION FOR SEQ ID NO:  21:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  32 BASE PAIRS
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  SINGLE
;       TOPOLOGY:  LINEAR
;     MOLECULE TYPE:  Oligonucleotide
US-08-875-272-21


  Query Match             78.8%;  Score 13.4;  DB 2;  Length 32;
  Best Local Similarity   93.3%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 ggccccccatggtgga 15
           |||| ||||||||||
Db      22 GGCCGCCATGGTGGA 8


RESULT  11
US-08-903-396-21/c
; Sequence 21, Application US/08903396
; Patent No. 5968797
;  GENERAL INFORMATION:
;    APPLICANT:  NI, ET AL.
;    TITLE OF INVENTION:  Ubiquitin Conjugating Enzymes
;    TITLE OF INVENTION:  7, 8 and 9
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/903,396
;      FILING DATE:  22-JUL-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/464,342
;      FILING DATE:  5-JUN-1995
;      APPLICATION NUMBER:  PCT/US95/01250
;      FILING DATE:  31-JAN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MULLINS, J.G.
;      REGISTRATION NUMBER:  33,073
;      REFERENCE/DOCKET NUMBER:  325800-373
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  32 BASE PAIRS
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  SINGLE
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  Oligonucleotide
US-08-903-396-21


  Query Match             78.8%;  Score 13.4;  DB 2;  Length 32;
  Best Local Similarity   93.3%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 ggccccccatggtgga 15
           |||| ||||||||||
Db      22 GGCCGCCATGGTGGA 8


RESULT  12
US-08-464-342-15/c
; Sequence 15, Application US/08464342
; Patent No. 5650313
;  GENERAL INFORMATION:
;    APPLICANT:  NI, ET AL.
;    TITLE OF INVENTION:  Ubiquitin Conjugating Enzymes
;    TITLE OF INVENTION:  7, 8 and 9
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/464,342
;      FILING DATE:  5 JUN 95
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/01250
;      FILING DATE:  31 JAN 95
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MULLINS, J.G.
;      REGISTRATION NUMBER:  33,073
;      REFERENCE/DOCKET NUMBER:  325800-373
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  33 BASE PAIRS
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  SINGLE
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  Oligonucleotide
US-08-464-342-15


  Query Match             78.8%;  Score 13.4;  DB 1;  Length 33;
  Best Local Similarity   93.3%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 ggccccccatggtgga 15
           |||| ||||||||||
```

```
Db      22 GGCCGCCATGGTGGA 8


RESULT  13
US-08-464-604A-18/c
; Sequence 18, Application US/08464604A
; Patent No. 5849286
;  GENERAL INFORMATION:
;    APPLICANT:  NI, JIAN
;    APPLICANT:  GENTZ, REINER
;    APPLICANT:  ADAMS, MARK D
;    TITLE OF INVENTION:  UBIQUITIN CONJUGATING ENZYMES 7, 8 AND 9
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
;      ADDRESSEE:  STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/464,604A
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FERRARO, GREGORY D
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-419
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  33 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-464-604A-18


  Query Match             78.8%;  Score 13.4;  DB 2;  Length 33;
  Best Local Similarity   93.3%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 ggccccccatggtgga 15
          |||| ||||||||||
Db      22 GGCCGCCATGGTGGA 8


RESULT  14
US-08-875-272-15/c
; Sequence 15, Application US/08875272
; Patent No. 5945321
;  GENERAL INFORMATION:
;    APPLICANT:  NI, ET AL.
;    TITLE OF INVENTION:  Ubiquitin Conjugating Enzymes 7, 8 and 9
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/875,272
;      FILING DATE:  Concurrently
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FERRARO, GREGORY D.
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-244
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  33 BASE PAIRS
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  SINGLE
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  Oligonucleotide
US-08-875-272-15


  Query Match             78.8%;  Score 13.4;  DB 2;  Length 33;
  Best Local Similarity   93.3%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 ggccccccatggtgga 15
          |||| ||||||||||
Db      22 GGCCGCCATGGTGGA 8


RESULT  15
US-08-903-396-15/c
; Sequence 15, Application US/08903396
; Patent No. 5968797
;  GENERAL INFORMATION:
;    APPLICANT:  NI, ET AL.
;    TITLE OF INVENTION:  Ubiquitin Conjugating Enzymes
;    TITLE OF INVENTION:  7, 8 and 9
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/903,396
;      FILING DATE:  22-JUL-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/464,342
;      FILING DATE:  5-JUN-1995
;      APPLICATION NUMBER:  PCT/US95/01250
;      FILING DATE:  31-JAN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MULLINS, J.G.
;      REGISTRATION NUMBER:  33,073
;      REFERENCE/DOCKET NUMBER:  325800-373
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
```

```
;       TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  15:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  33 BASE PAIRS
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  SINGLE
;       TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  Oligonucleotide
US-08-903-396-15


  Query Match             78.8%;  Score 13.4;  DB 2;  Length 33;
  Best Local Similarity   93.3%;  Pred. No. 3.5e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 ggcccccatggtgga 15
           |||| ||||||||||
Db      22 GGCCGCCATGGTGGA 8


Search completed: March 23, 2001, 15:55:07
Job time: 35666 sec
```

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 23, 2001, 13:36:24 ; Search time 2149.74 Seconds
(without alignments)
33.329 Million cell updates/sec

Title: US-09-554-267-4
Perfect score: 14
Sequence: 1 ggcccccatggtgg 14

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1118133 seqs, 2558875100 residues

Total number of hits satisfying chosen parameters: 349344

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba1:*
2: gb_ba2:*
3: gb_om:*
4: gb_ov:*
5: gb_ph:*
6: gb_pl1:*
7: gb_pl2:*
8: gb_pr1:*
9: gb_pr2:*
10: gb_pr3:*
11: gb_ro:*
12: gb_sy:*
13: gb_un:*
14: em_fun:*
15: em_hum1:*
16: em_hum2:*
17: em_in:*
18: em_om:*
19: em_or:*
20: em_ov:*
21: em_pat:*
22: em_ph:*
23: em_pl:*
24: em_ro:*
25: em_sts:*
26: em_sy:*
27: em_un:*
28: em_vi:*
29: gb_ba3:*
30: gb_in1:*
31: gb_in2:*
32: gb_in3:*
33: gb_pl3:*
34: gb_pr4:*
35: em_ba1:*
36: em_ba2:*
37: em_htg1:*
38: em_htg2:*
39: em_htg3:*
40: em_htg4:*
41: em_htg5:*
42: em_htg6:*
43: em_htg7:*
44: em_htg8:*
45: em_htg9:*
46: em_htg10:*
47: em_hum3:*
48: em_hum4:*
49: em_hum5:*
50: em_hum6:*
51: gb_pr5:*
52: gb_pr6:*
53: gb_pr7:*
54: gb_htg1:*
55: gb_htg2:*
56: gb_htg3:*
57: gb_htg4:*
58: gb_htg5:*
59: gb_htg6:*
60: gb_htg7:*
61: gb_htg8:*
62: gb_htg9:*
63: gb_htg10:*
64: gb_htg11:*
65: gb_htg12:*
66: gb_htg13:*
67: gb_htg14:*
68: gb_htg15:*
69: gb_htg16:*
70: gb_htg17:*
71: gb_htg18:*
72: gb_htg19:*
73: gb_htg20:*
74: gb_htg21:*
75: gb_htg22:*
76: gb_htg23:*
77: gb_sts1:*
78: gb_sts2:*
79: gb_vi1:*
80: gb_vi2:*
81: gb_pat1:*
82: gb_pat2:*
83: em_htg0:*
84: gb_htg24:*
85: gb_pr8:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		14	100.0	14	13	AX022896	AX022896 Sequence
2		14	100.0	14	13	AX022915	AX022915 Sequence
3		14	100.0	14	13	AX022934	AX022934 Sequence
4		14	100.0	14	13	AX030484	AX030484 Sequence
5		14	100.0	14	13	AX030503	AX030503 Sequence
6		14	100.0	14	13	AX030522	AX030522 Sequence
7		14	100.0	17	13	AX022895	AX022895 Sequence
8		14	100.0	17	13	AX022914	AX022914 Sequence
9		14	100.0	17	13	AX022933	AX022933 Sequence
10		14	100.0	17	13	AX030483	AX030483 Sequence
11		14	100.0	17	13	AX030502	AX030502 Sequence
12		14	100.0	17	13	AX030521	AX030521 Sequence
c 13		13	92.9	24	82	I94998	I94998 Sequence 7
c 14		12.4	88.6	29	81	E16765	E16765 PCR primer
c 15		12.4	88.6	32	81	AR064674	AR064674 Sequence
c 16		12.4	88.6	32	81	AR080568	AR080568 Sequence
c 17		12.4	88.6	32	81	I56807	I56807 Sequence 21
c 18		12.4	88.6	33	81	AR064668	AR064668 Sequence
c 19		12.4	88.6	33	81	AR080562	AR080562 Sequence
c 20		12.4	88.6	33	81	I56801	I56801 Sequence 15
c 21		12.4	88.6	41	81	AR096932	AR096932 Sequence

c	22	12	85.7	24	81	AR063265	AR063265 Sequence
c	23	12	85.7	33	81	A36006	A36006 Sequence 5
c	24	12	85.7	43	81	A56908	A56908 Sequence 4
c	25	12	85.7	47	81	A38861	A38861 Sequence 15
c	26	12	85.7	47	81	A73050	A73050 Sequence 26
c	27	12	85.7	47	81	A73142	A73142 Sequence 26
c	28	11.4	81.4	25	81	AR086739	AR086739 Sequence
c	29	11.4	81.4	33	81	AR004878	AR004878 Sequence
c	30	11.4	81.4	33	81	AR020560	AR020560 Sequence
	31	11.4	81.4	36	12	AX012335	AX012335 Sequence
c	32	11.4	81.4	36	51	AX021210	AX021210 Sequence
c	33	11.4	81.4	36	81	A94277	A94277 Sequence 30
c	34	11.4	81.4	37	81	AR018953	AR018953 Sequence
c	35	11.4	81.4	41	81	AR096921	AR096921 Sequence
c	36	11.4	81.4	46	81	A07643	A07643 Synthetic o
	37	11	78.6	11	13	AX022910	AX022910 Sequence
	38	11	78.6	11	13	AX022929	AX022929 Sequence
	39	11	78.6	11	13	AX022948	AX022948 Sequence
	40	11	78.6	11	13	AX030498	AX030498 Sequence
	41	11	78.6	11	13	AX030517	AX030517 Sequence
	42	11	78.6	11	13	AX030536	AX030536 Sequence
c	43	11	78.6	12	81	A36015	A36015 Sequence 14
	44	11	78.6	14	13	AX022897	AX022897 Sequence
	45	11	78.6	14	13	AX022916	AX022916 Sequence

ALIGNMENTS

```
RESULT   1
AX022896
LOCUS       AX022896       14 bp    DNA             UNA       07-SEP-2000
DEFINITION  Sequence 4 from Patent WO9925819.
ACCESSION   AX022896
VERSION     AX022896.1  GI:10046387
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Uhlmann,E., Weiser,C. and Peyman,A.
  TITLE     Antisense oligonucleotides against tenascin for treating vitiligo
  JOURNAL   Patent: WO 9925819-A 27-MAY-1999;
            UHLMANN EUGEN (DE); WEISER CAROLINE (DE); HOECHST MARION ROUSSEL DE
            GMBH (DE); PEYMAN ANUSCHIRWAN (DE)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unidentified"
                     /db_xref="taxon:32644"
     exon            1. .14
BASE COUNT        1 a      5 c      6 g      2 t
ORIGIN


  Query Match             100.0%;  Score 14;  DB 13;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggcccccatggtgg 14
          ||||||||||||||
Db      1 GGCCCCCATGGTGG 14


RESULT   2
AX022915
LOCUS       AX022915       14 bp    DNA             UNA       07-SEP-2000
DEFINITION  Sequence 23 from Patent WO9925819.
ACCESSION   AX022915
VERSION     AX022915.1  GI:10046407
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Uhlmann,E., Weiser,C. and Peyman,A.
  TITLE     Antisense oligonucleotides against tenascin for treating vitiligo
  JOURNAL   Patent: WO 9925819-A 27-MAY-1999;
            UHLMANN EUGEN (DE); WEISER CAROLINE (DE); HOECHST MARION ROUSSEL DE
            GMBH (DE); PEYMAN ANUSCHIRWAN (DE)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        1 a      5 c      6 g      2 t
ORIGIN


  Query Match             100.0%;  Score 14;  DB 13;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggcccccatggtgg 14
          ||||||||||||||
Db      1 GGCCCCCATGGTGG 14


RESULT   3
AX022934
LOCUS       AX022934       14 bp    DNA             UNA       07-SEP-2000
DEFINITION  Sequence 42 from Patent WO9925819.
ACCESSION   AX022934
VERSION     AX022934.1  GI:10046427
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Uhlmann,E., Weiser,C. and Peyman,A.
  TITLE     Antisense oligonucleotides against tenascin for treating vitiligo
  JOURNAL   Patent: WO 9925819-A 27-MAY-1999;
            UHLMANN EUGEN (DE); WEISER CAROLINE (DE); HOECHST MARION ROUSSEL DE
            GMBH (DE); PEYMAN ANUSCHIRWAN (DE)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        1 a      5 c      6 g      2 t
ORIGIN


  Query Match             100.0%;  Score 14;  DB 13;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggcccccatggtgg 14
          ||||||||||||||
Db      1 GGCCCCCATGGTGG 14


RESULT   4
AX030484
LOCUS       AX030484       14 bp    DNA             UNA       20-SEP-2000
DEFINITION  Sequence 4 from Patent DE19750702.
ACCESSION   AX030484
VERSION     AX030484.1  GI:10278041
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Peyman,A.D., Uhlmann,E.D. and Weiser,C.D.
  TITLE     Antisense oligonucleotides that bind to sequences encoding human
            tenascin for treating depigmentation, cancer, inflammation and
            cardiovascular disease
  JOURNAL   Patent: DE 19750702-A 27-MAY-1999;
            HOECHST MARION ROUSSEL DE GMBH (DE)
```

```
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unidentified"
                     /db_xref="taxon:32644"
     exon            1. .14
BASE COUNT        1 a      5 c      6 g      2 t
ORIGIN


  Query Match             100.0%;  Score 14;  DB 13;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggccccccatggtgg 14
          ||||||||||||||
Db      1 GGCCCCCATGGTGG 14


RESULT   5
AX030503
LOCUS       AX030503       14 bp    DNA             UNA       20-SEP-2000
DEFINITION  Sequence 23 from Patent DE19750702.
ACCESSION   AX030503
VERSION     AX030503.1  GI:10278060
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Peyman,A.D., Uhlmann,E.D. and Weiser,C.D.
  TITLE     Antisense oligonucleotides that bind to sequences encoding human
            tenascin for treating depigmentation, cancer, inflammation and
            cardiovascular disease
  JOURNAL   Patent: DE 19750702-A 27-MAY-1999;
            HOECHST MARION ROUSSEL DE GMBH (DE)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        1 a      5 c      6 g      2 t
ORIGIN


  Query Match             100.0%;  Score 14;  DB 13;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggccccccatggtgg 14
          ||||||||||||||
Db      1 GGCCCCCATGGTGG 14


RESULT   6
AX030522
LOCUS       AX030522       14 bp    DNA             UNA       20-SEP-2000
DEFINITION  Sequence 42 from Patent DE19750702.
ACCESSION   AX030522
VERSION     AX030522.1  GI:10278079
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Peyman,A.D., Uhlmann,E.D. and Weiser,C.D.
  TITLE     Antisense oligonucleotides that bind to sequences encoding human
            tenascin for treating depigmentation, cancer, inflammation and
            cardiovascular disease
  JOURNAL   Patent: DE 19750702-A 27-MAY-1999;
            HOECHST MARION ROUSSEL DE GMBH (DE)
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        1 a      5 c      6 g      2 t
ORIGIN


  Query Match             100.0%;  Score 14;  DB 13;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggccccccatggtgg 14
          ||||||||||||||
Db      1 GGCCCCCATGGTGG 14


RESULT   7
AX022895
LOCUS       AX022895       17 bp    DNA             UNA       07-SEP-2000
DEFINITION  Sequence 3 from Patent WO9925819.
ACCESSION   AX022895
VERSION     AX022895.1  GI:10046386
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Uhlmann,E., Weiser,C. and Peyman,A.
  TITLE     Antisense oligonucleotides against tenascin for treating vitiligo
  JOURNAL   Patent: WO 9925819-A 27-MAY-1999;
            UHLMANN EUGEN (DE); WEISER CAROLINE (DE); HOECHST MARION ROUSSEL DE
            GMBH (DE); PEYMAN ANUSCHIRWAN (DE)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /db_xref="taxon:32644"
     exon            1. .17
BASE COUNT        2 a      5 c      8 g      2 t
ORIGIN


  Query Match             100.0%;  Score 14;  DB 13;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggccccccatggtgg 14
          ||||||||||||||
Db      1 GGCCCCCATGGTGG 14


RESULT   8
AX022914
LOCUS       AX022914       17 bp    DNA             UNA       07-SEP-2000
DEFINITION  Sequence 22 from Patent WO9925819.
ACCESSION   AX022914
VERSION     AX022914.1  GI:10046406
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Uhlmann,E., Weiser,C. and Peyman,A.
  TITLE     Antisense oligonucleotides against tenascin for treating vitiligo
  JOURNAL   Patent: WO 9925819-A 27-MAY-1999;
            UHLMANN EUGEN (DE); WEISER CAROLINE (DE); HOECHST MARION ROUSSEL DE
            GMBH (DE); PEYMAN ANUSCHIRWAN (DE)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        2 a      5 c      8 g      2 t
ORIGIN


  Query Match             100.0%;  Score 14;  DB 13;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+03;
```

```
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggccccccatggtgg 14
          ||||||||||||||
Db      1 GGCCCCCCATGGTGG 14


RESULT   9
AX022933
LOCUS       AX022933       17 bp    DNA             UNA       07-SEP-2000
DEFINITION  Sequence 41 from Patent WO9925819.
ACCESSION   AX022933
VERSION     AX022933.1  GI:10046426
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Uhlmann,E., Weiser,C. and Peyman,A.
  TITLE     Antisense oligonucleotides against tenascin for treating vitiligo
  JOURNAL   Patent: WO 9925819-A 27-MAY-1999;
            UHLMANN EUGEN (DE); WEISER CAROLINE (DE); HOECHST MARION ROUSSEL DE
            GMBH (DE); PEYMAN ANUSCHIRWAN (DE)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        2 a      5 c      8 g      2 t
ORIGIN


  Query Match             100.0%;  Score 14;  DB 13;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggccccccatggtgg 14
          ||||||||||||||
Db      1 GGCCCCCCATGGTGG 14


RESULT  10
AX030483
LOCUS       AX030483       17 bp    DNA             UNA       20-SEP-2000
DEFINITION  Sequence 3 from Patent DE19750702.
ACCESSION   AX030483
VERSION     AX030483.1  GI:10278040
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Peyman,A.D., Uhlmann,E.D. and Weiser,C.D.
  TITLE     Antisense oligonucleotides that bind to sequences encoding human
            tenascin for treating depigmentation, cancer, inflammation and
            cardiovascular disease
  JOURNAL   Patent: DE 19750702-A 27-MAY-1999;
            HOECHST MARION ROUSSEL DE GMBH (DE)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /db_xref="taxon:32644"
     exon            1. .17
BASE COUNT        2 a      5 c      8 g      2 t
ORIGIN


  Query Match             100.0%;  Score 14;  DB 13;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggccccccatggtgg 14
          ||||||||||||||
Db      1 GGCCCCCCATGGTGG 14


RESULT  11
AX030502
LOCUS       AX030502       17 bp    DNA             UNA       20-SEP-2000
DEFINITION  Sequence 22 from Patent DE19750702.
ACCESSION   AX030502
VERSION     AX030502.1  GI:10278059
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Peyman,A.D., Uhlmann,E.D. and Weiser,C.D.
  TITLE     Antisense oligonucleotides that bind to sequences encoding human
            tenascin for treating depigmentation, cancer, inflammation and
            cardiovascular disease
  JOURNAL   Patent: DE 19750702-A 27-MAY-1999;
            HOECHST MARION ROUSSEL DE GMBH (DE)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        2 a      5 c      8 g      2 t
ORIGIN


  Query Match             100.0%;  Score 14;  DB 13;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggccccccatggtgg 14
          ||||||||||||||
Db      1 GGCCCCCCATGGTGG 14


RESULT  12
AX030521
LOCUS       AX030521       17 bp    DNA             UNA       20-SEP-2000
DEFINITION  Sequence 41 from Patent DE19750702.
ACCESSION   AX030521
VERSION     AX030521.1  GI:10278078
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Peyman,A.D., Uhlmann,E.D. and Weiser,C.D.
  TITLE     Antisense oligonucleotides that bind to sequences encoding human
            tenascin for treating depigmentation, cancer, inflammation and
            cardiovascular disease
  JOURNAL   Patent: DE 19750702-A 27-MAY-1999;
            HOECHST MARION ROUSSEL DE GMBH (DE)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        2 a      5 c      8 g      2 t
ORIGIN


  Query Match             100.0%;  Score 14;  DB 13;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggccccccatggtgg 14
          ||||||||||||||
Db      1 GGCCCCCCATGGTGG 14


RESULT  13
I94998/c
LOCUS       I94998         24 bp    DNA             PAT       01-DEC-1998
```

```
DEFINITION  Sequence 7 from patent US 5731415.
ACCESSION   I94998
VERSION     I94998.1  GI:3939468
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Gazzano-Santoro,H., Theofan,G. and Trown,P.W.
  TITLE     Lipopolysaccharide binding protein derivatives
  JOURNAL   Patent: US 5731415-A 7 24-MAR-1998;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
BASE COUNT       4 a      7 c      8 g      5 t
ORIGIN


  Query Match           92.9%;  Score 13;  DB 82;  Length 24;
  Best Local Similarity  100.0%;  Pred. No. 1.1e+04;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggcccccatggtg 13
          |||||||.||||||
Db     21 GGCCCCCATGGTG 9


RESULT  14
E16765/c
LOCUS       E16765         29 bp    DNA             PAT       28-JUL-1999
DEFINITION  PCR primer for gaining curculin gene.
ACCESSION   E16765
VERSION     E16765.1  GI:5711448
KEYWORDS    JP 1998215884-A/2.
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Kurihara,Y., Arai,S., Anzai,H., Katsumata,K., Yamashita,H. and
            Sugiyama,H. .
  TITLE     SOURNESS REPRESANT, PLASMID FOR PLANT, TRANSFORMED CELL AND PLANT,
            AND PRODUCTION OF CURCULIN
  JOURNAL   Patent: JP 1998215884-A 18-AUG-1998;
            KURIHARA YOSHIE, ARAI SOICHI, MEIJI SEIKA KAISHA LTD, ASAHI DENKA
            KOGYO KK
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1998215884-A/2
            PD   18-AUG-1998
            PF   05-DEC-1997 JP 1997352320
            PR   06-DEC-1996 JP 96P   342706
            PI   KURIHARA YOSHIE, ARAI SOICHI, ANZAI HIROYUKI, KATSUMATA
            KAZUKO, PI   YAMASHITA HARUYUKI, SUGIYAMA HIROSHI
            PC   C12N15/09,A01H5/00,A23J3/14,A23L1/00,A23L1/22,C07K14/415, PC
            C12N5/10,
            PC   C12P21/02,(C12N15/09,C12R1:91),(C12N5/10,C12R1:91),(C12P21/02,
            PC   C12R1:91);
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: No;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .29
            FT                   /organism='Artificial sequecnes'.
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT       5 a      9 c      7 g      8 t
ORIGIN


  Query Match           88.6%;  Score 12.4;  DB 81;  Length 29;
  Best Local Similarity  92.9%;  Pred. No. 2.4e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 ggcccccatggtgg 14
          |||| |||||||||
Db     18 GGCCGCCATGGTGG 5


RESULT  15
AR064674/c
LOCUS       AR064674       32 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 24 from patent US 5849286.
ACCESSION   AR064674
VERSION     AR064674.1  GI:5994890
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Ni,J., Gentz,R. and Adams,M.D.
  TITLE     Ubiquitin conjugating enzymes 7,8 and 9
  JOURNAL   Patent: US 5849286-A 24 15-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="unknown"
BASE COUNT       6 a      11 c     13 g      2 t
ORIGIN


  Query Match           88.6%;  Score 12.4;  DB 81;  Length 32;
  Best Local Similarity  92.9%;  Pred. No. 2.3e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 ggcccccatggtgg 14
          |||| |||||||||
Db     22 GGCCGCCATGGTGG 9


Search completed: March 23, 2001, 13:36:25
Job time: 27628 sec
```

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 23, 2001, 16:04:32 ; Search time 551.33 Seconds
(without alignments)
9.539 Million cell updates/sec

Title: US-09-554-267-4
Perfect score: 14
Sequence: 1 ggcccccatggtgg 14

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 624296

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_36:*
1: /cgn2_2/gcgdata/geneseq/geneseqn/NA1980.DAT:*
2: /cgn2_2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
3: /cgn2_2/gcgdata/geneseq/geneseqn/NA1982.DAT:*
4: /cgn2_2/gcgdata/geneseq/geneseqn/NA1983.DAT:*
5: /cgn2_2/gcgdata/geneseq/geneseqn/NA1984.DAT:*
6: /cgn2_2/gcgdata/geneseq/geneseqn/NA1985.DAT:*
7: /cgn2_2/gcgdata/geneseq/geneseqn/NA1986.DAT:*
8: /cgn2_2/gcgdata/geneseq/geneseqn/NA1987.DAT:*
9: /cgn2_2/gcgdata/geneseq/geneseqn/NA1988.DAT:*
10: /cgn2_2/gcgdata/geneseq/geneseqn/NA1989.DAT:*
11: /cgn2_2/gcgdata/geneseq/geneseqn/NA1990.DAT:*
12: /cgn2_2/gcgdata/geneseq/geneseqn/NA1991.DAT:*
13: /cgn2_2/gcgdata/geneseq/geneseqn/NA1992.DAT:*
14: /cgn2_2/gcgdata/geneseq/geneseqn/NA1993.DAT:*
15: /cgn2_2/gcgdata/geneseq/geneseqn/NA1994.DAT:*
16: /cgn2_2/gcgdata/geneseq/geneseqn/NA1995.DAT:*
17: /cgn2_2/gcgdata/geneseq/geneseqn/NA1996.DAT:*
18: /cgn2_2/gcgdata/geneseq/geneseqn/NA1997.DAT:*
19: /cgn2_2/gcgdata/geneseq/geneseqn/NA1998.DAT:*
20: /cgn2_2/gcgdata/geneseq/geneseqn/NA1999.DAT:*
21: /cgn2_2/gcgdata/geneseq/geneseqn/NA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		14	100.0	18	15	Q77634	Ribonucleotide to
2	c	14	100.0	18	15	Q77620	Antisense polynucl
3	c	14	100.0	18	15	Q77648	Antisense ribonucl
4		14	100.0	18	15	Q76393	Polynucleotide to
5		14	100.0	24	15	Q77617	Polynucleotide to
6	c	14	100.0	24	15	Q77659	Antisense ribonucl
7	c	14	100.0	24	15	Q77631	Antisense polynucl
8		14	100.0	24	15	Q77645	Ribonucleotide to
9	c	14	100.0	36	15	Q76387	Tenascin gene cons
10		14	100.0	36	15	Q76386	Tenascin gene cons
11	c	14	100.0	36	15	Q77661	Tenascin gene mRNA
12		14	100.0	36	15	Q77662	Tenascin gene mRNA
13	c	13	92.9	24	16	Q80830	Lipopolysaccharide
14	c	13	92.9	24	19	V10334	Human rLBP PCR pri
15	c	13	92.9	24	21	Z61427	PCR primer for DNA
16		13	92.9	27	20	X88424	IBV M protein PCR
17	c	13	92.9	34	17	T10560	Serum paraoxonase
18	c	12.4	88.6	27	18	T90893	5' primer for epid
19	c	12.4	88.6	31	18	T68725	Human osteo antivi
20	c	12.4	88.6	31	19	V45332	Human extracellula
21	c	12.4	88.6	31	21	Z58151	Human FAST-1 gene
22	c	12.4	88.6	32	17	T39712	Ubiquitin conjugat
23	c	12.4	88.6	32	18	T79829	Primer used for am
24	c	12.4	88.6	32	20	Z25321	Human ubiquitin co
25	c	12.4	88.6	32	20	V82882	5' PCR primer used
26	c	12.4	88.6	33	17	T39706	Ubiquitin conjugat
27	c	12.4	88.6	33	18	T79823	Primer used for am
28	c	12.4	88.6	33	20	Z25315	Human ubiquitin co
29	c	12.4	88.6	33	20	V82876	5' PCR primer used
30	c	12.4	88.6	35	20	Z33020	Human ATR-5 L chai
31	c	12.4	88.6	35	20	X36573	PCR primer for hum
32	c	12.4	88.6	41	18	T97210	Kappa chain variab
33		12	85.7	21	15	Q77638	Ribonucleotide to
34		12	85.7	21	15	Q77642	Ribonucleotide to
35		12	85.7	21	15	Q77614	Polynucleotide to
36	c	12	85.7	21	15	Q77656	Antisense ribonucl
37	c	12	85.7	21	15	Q77624	Antisense polynucl
38	c	12	85.7	21	15	Q77628	Antisense polynucl
39	c	12	85.7	21	15	Q77652	Antisense ribonucl
40		12	85.7	21	15	Q76397	Polynucleotide to
41		12	85.7	24	15	Q77639	Ribonucleotide to
42		12	85.7	24	15	Q77641	Ribonucleotide to
43		12	85.7	24	15	Q76400	Polynucleotide to
44	c	12	85.7	24	15	Q77655	Antisense ribonucl
45	c	12	85.7	24	15	Q77625	Antisense polynucl

ALIGNMENTS

RESULT 1
Q77634
ID Q77634 standard; RNA; 18 BP.
XX
AC Q77634;
XX
DT 02-JUN-1995 (first entry)
XX
DE Ribonucleotide to tenascin gene consensus mRNA initiation site -9-+9.
XX
KW Antisense; polynucleotide; sense strand; tenascin; complementary;
KW consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW proliferation; growth stimulatory; transcription; vascular stenosis;
KW post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW organ transplant; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_difference 1..18
FT /*tag= a
FT /note= "phosphodiester bonds between nucleotides
FT may be replaced by phosphorothioate bonds'
XX
PN WO9421664-A.
XX
PD 29-SEP-1994.
XX
PF 24-MAR-1994; 94WO-US03206.
XX
PR 25-MAR-1993; 93US-0037025.
XX
PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI Denner LA, Dixon RAF, Rege AA, Stacy DL;

```
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 5; Page 47; 64pp; English.
XX
CC   A series of polynucleotides, either DNA (Q76388 and Q76392-400 and
CC   Q77614-18) or RNA (Q76390 and Q77633-46), directed against the consensus
CC   mRNA initiation site sequence (Q77661) for the tenascin gene.  The
CC   polynucleotides are based on the degenerate sequence (Q76386) of the
CC   tenascin gene.  Tenascin is an extracellular matrix glycoprotein
CC   consisting six disulphide-linked subunits, each having molecular mass of
CC   190-250 kDa.  Tenascin may be important for smooth muscle cell
CC   proliferation as the protein has growth stimulatory activity.  The
CC   polynucleotides can be used to inhibit transcription of the gene or
CC   translation of the mRNA encoding tenascin. The method is applicable to a
CC   number of diseases where the proliferation of smooth muscle is involved
CC   e.g. vascular stenosis, post-angioplasty restenosis and other
CC   non-angioplasty procedures such as cardiac hypertrophy, vascular surgery
CC   and organ transplant.
XX
SQ   Sequence 18 BP; 2 A; 5 C; 8 G; 3 U; 0 other;


  Query Match             100.0%;  Score 14;  DB 15;  Length 18;
  Best Local Similarity   85.7%;  Pred. No. 54;
  Matches   12;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggcccccatggtgg 14
          ||||||||:||:||
Db      1 ggcccccauggugg 14


RESULT   2
Q77620/c
ID   Q77620 standard; DNA; 18 BP.
XX
AC   Q77620;
XX
DT   01-JUN-1995  (first entry)
XX
DE   Antisense polynucleotide binds to tenascin gene consensus at -9-+9.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..18
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                          may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 10; Page 44; 64pp; English.
XX
CC   A series of antisense polynucleotides, either DNA (Q76388 and Q77619-32)
CC   or RNA (Q76390 and Q77647-60) directed against the sense strand of the
CC   gene encoding tenascin.  The polynucleotides are based on the
CC   complementary sequence (Q76386) of the consensus mRNA initiation site
CC   sequence (Q77661) for the tenascin gene.  Tenascin is an extracellular
CC   matrix glycoprotein consisting six disulphide-linked subunits, each
CC   having molecular mass of 190-250 kDa.  Tenascin may be important for
CC   smooth muscle cell proliferation as the protein has growth stimulatory
CC   activity.  The polynucleotides can be used to inhibit transcription
CC   of the gene or translation of the mRNA encoding tenascin.  The method is
CC   applicable to a number of diseases where the proliferation of smooth
CC   muscle is involved e.g. vascular stenosis, post-angioplasty restenosis
CC   and other non-angioplasty procedures such as cardiac hypertrophy,
CC   vascular surgery and organ transplant.
XX
SQ   Sequence 18 BP; 3 A; 8 C; 5 G; 2 T; 0 other;


  Query Match             100.0%;  Score 14;  DB 15;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggcccccatggtgg 14
          ||||||||||||||
Db     18 GGCCCCCATGGTGG 5


RESULT   3
Q77648/c
ID   Q77648 standard; RNA; 18 BP.
XX
AC   Q77648;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Antisense ribonucleotide binds to tenascin gene consensus at -9-+9.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..18
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                          may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
```

```
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 10; Page 51; 64pp; English.
XX
CC   A series of antisense polynucleotides, either DNA (Q76388 and Q77619-32)
CC   or RNA (Q76390 and Q77647-60) directed against the sense strand of the
CC   gene encoding tenascin.  The polynucleotides are based on the
CC   complementary sequence (Q76386) of the consensus mRNA initiation site
CC   sequence (Q77661) for the tenascin gene.  Tenascin is an extracellular
CC   matrix glycoprotein consisting six disulphide-linked subunits, each
CC   having molecular mass of 190-250 kDa.  Tenascin may be important for
CC   smooth muscle cell proliferation as the protein has growth stimulatory
CC   activity.  The polynucleotides can be used to inhibit transcription
CC   of the gene or translation of the mRNA encoding tenascin.  The method is
CC   applicable to a number of diseases where the proliferation of smooth
CC   muscle is involved e.g. vascular stenosis, post-angioplasty restenosis
CC   and other non-angioplasty procedures such as cardiac hypertrophy,
CC   vascular surgery and organ transplant.
XX
SQ   Sequence 18 BP; 3 A; 8 C; 5 G; 2 U; 0 other;


  Query Match             100.0%;  Score 14;  DB 15;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggcccccatggtgg 14
          ||||||||||||||
Db     18 GGCCCCCATGGTGG 5


RESULT   4
Q76393
ID   Q76393 standard; DNA; 18 BP.
XX
AC   Q76393;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Polynucleotide to tenascin gene consensus mRNA initiation site -9-+9.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..18
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                           may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 5; Page 40; 64pp; English.
XX
CC   A series of polynucleotides, either DNA (Q76388 and Q76392-400 and
CC   Q77614-18) or RNA (Q76390 and Q77633-46), directed against the consensus
CC   mRNA initiation site sequence (Q77661) for the tenascin gene.  The
CC   polynucleotides are based on the degenerate sequence (Q76386) of the
CC   tenascin gene.  Tenascin is an extracellular matrix glycoprotein
CC   consisting six disulphide-linked subunits, each having molecular mass of
CC   190-250 kDa.  Tenascin may be important for smooth muscle cell
CC   proliferation as the protein has growth stimulatory activity.  The
CC   polynucleotides can be used to inhibit transcription of the gene or
CC   translation of the mRNA encoding tenascin. The method is applicable to a
CC   number of diseases where the proliferation of smooth muscle is involved
CC   e.g. vascular stenosis, post-angioplasty restenosis and other
CC   non-angioplasty procedures such as cardiac hypertrophy, vascular surgery
CC   and organ transplant.
XX
SQ   Sequence 18 BP; 2 A; 5 C; 8 G; 3 T; 0 other;


  Query Match             100.0%;  Score 14;  DB 15;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggcccccatggtgg 14
          ||||||||||||||
Db      1 ggcccccatggtgg 14


RESULT   5
Q77617
ID   Q77617 standard; DNA; 24 BP.
XX
AC   Q77617;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Polynucleotide to tenascin gene consensus mRNA initiation site -6-+18.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..24
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                           may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 5; Page 43; 64pp; English.
```

```
XX
CC   A series of polynucleotides, either DNA (Q76388 and Q76392-400 and
CC   Q77614-18) or RNA (Q76390 and Q77633-46), directed against the consensus
CC   mRNA initiation site sequence (Q77661) for the tenascin gene.  The
CC   polynucleotides are based on the degenerate sequence (Q76386) of the
CC   tenascin gene.  Tenascin is an extracellular matrix glycoprotein
CC   consisting six disulphide-linked subunits, each having molecular mass of
CC   190-250 kDa.  Tenascin may be important for smooth muscle cell
CC   proliferation as the protein has growth stimulatory activity.  The
CC   polynucleotides can be used to inhibit transcription of the gene or
CC   translation of the mRNA encoding tenascin. The method is applicable to a
CC   number of diseases where the proliferation of smooth muscle is involved
CC   e.g. vascular stenosis, post-angioplasty restenosis and other
CC   non-angioplasty procedures such as cardiac hypertrophy, vascular surgery
CC   and organ transplant.
XX
SQ   Sequence 24 BP; 4 A; 7 C; 8 G; 5 T; 0 other;


  Query Match             100.0%;  Score 14;  DB 15;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 55;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggccccccatggtgg 14
          ||||||||||||||
Db     10 ggccccccatggtgg 23


RESULT   6
Q77659/c
ID   Q77659 standard; RNA; 24 BP.
XX
AC   Q77659;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Antisense ribonucleotide binds to tenascin gene consensus at -6-+18.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..24
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                           may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 10; Page 53; 64pp; English.
XX
CC   A series of antisense polynucleotides, either DNA (Q76388 and Q77619-32)
CC   or RNA (Q76390 and Q77647-60) directed against the sense strand of the
CC   gene encoding tenascin.  The polynucleotides are based on the
CC   complementary sequence (Q76386) of the consensus mRNA initiation site
CC   sequence (Q77661) for the tenascin gene.  Tenascin is an extracellular
CC   matrix glycoprotein consisting six disulphide-linked subunits, each
CC   having molecular mass of 190-250 kDa.  Tenascin may be important for
CC   smooth muscle cell proliferation as the protein has growth stimulatory
CC   activity.  The polynucleotides can be used to inhibit transcription
CC   of the gene or translation of the mRNA encoding tenascin.  The method is
CC   applicable to a number of diseases where the proliferation of smooth
CC   muscle is involved e.g. vascular stenosis, post-angioplasty restenosis
CC   and other non-angioplasty procedures such as cardiac hypertrophy,
CC   vascular surgery and organ transplant.
XX
SQ   Sequence 24 BP; 5 A; 8 C; 7 G; 4 U; 0 other;


  Query Match             100.0%;  Score 14;  DB 15;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 55;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggccccccatggtgg 14
          ||||||||||||||
Db     15 GGCCCCCATGGTGG 2


RESULT   7
Q77631/c
ID   Q77631 standard; DNA; 24 BP.
XX
AC   Q77631;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Antisense polynucleotide binds to tenascin gene consensus at -6-+18.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..24
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                           may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 10; Page 46; 64pp; English.
XX
CC   A series of antisense polynucleotides, either DNA (Q76388 and Q77619-32)
CC   or RNA (Q76390 and Q77647-60) directed against the sense strand of the
CC   gene encoding tenascin.  The polynucleotides are based on the
```

```
CC   complementary sequence (Q76386) of the consensus mRNA initiation site
CC   sequence (Q77661) for the tenascin gene.  Tenascin is an extracellular
CC   matrix glycoprotein consisting six disulphide-linked subunits, each
CC   having molecular mass of 190-250 kDa.  Tenascin may be important for
CC   smooth muscle cell proliferation as the protein has growth stimulatory
CC   activity.  The polynucleotides can be used to inhibit transcription
CC   of the gene or translation of the mRNA encoding tenascin.  The method is
CC   applicable to a number of diseases where the proliferation of smooth
CC   muscle is involved e.g. vascular stenosis, post-angioplasty restenosis
CC   and other non-angioplasty procedures such as cardiac hypertrophy,
CC   vascular surgery and organ transplant.
XX
SQ   Sequence 24 BP; 5 A; 8 C; 7 G; 4 T; 0 other;


  Query Match             100.0%;  Score 14;  DB 15;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 55;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ggccccccatggtgg 14
           ||||||||||||||
Db      15 GGCCCCCATGGTGG 2


RESULT   8
Q77645
ID   Q77645 standard; RNA; 24 BP.
XX
AC   Q77645;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Ribonucleotide to tenascin gene consensus mRNA initiation site -6-+18.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..24
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                          may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 5; Page 50; 64pp; English.
XX
CC   A series of polynucleotides, either DNA (Q76388 and Q76392-400 and
CC   Q77614-18) or RNA (Q76390 and Q77633-46), directed against the consensus
CC   mRNA initiation site sequence (Q77661) for the tenascin gene.  The
CC   polynucleotides are based on the degenerate sequence (Q76386) of the
CC   tenascin gene.  Tenascin is an extracellular matrix glycoprotein
CC   consisting six disulphide-linked subunits, each having molecular mass of
CC   190-250 kDa.  Tenascin may be important for smooth muscle cell
CC   proliferation as the protein has growth stimulatory activity.  The
CC   polynucleotides can be used to inhibit transcription of the gene or
CC   translation of the mRNA encoding tenascin. The method is applicable to a
CC   number of diseases where the proliferation of smooth muscle is involved
CC   e.g. vascular stenosis, post-angioplasty restenosis and other
CC   non-angioplasty procedures such as cardiac hypertrophy, vascular surgery
CC   and organ transplant.
XX
SQ   Sequence 24 BP; 4 A; 7 C; 8 G; 5 U; 0 other;


  Query Match             100.0%;  Score 14;  DB 15;  Length 24;
  Best Local Similarity   85.7%;  Pred. No. 55;
  Matches   12;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ggccccccatggtgg 14
           |||||||:||:||
Db      10 ggcccccauggugg 23


RESULT   9
Q76387/c
ID   Q76387 standard; DNA; 36 BP.
XX
AC   Q76387;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Tenascin gene consensus DNA sequence sense strand.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..36
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                          may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 6; Page 39; 64pp; English.
XX
CC   A series of polynucleotides, either DNA (Q76389 and Q76392-400 and
CC   Q77614-18) or RNA (Q76391 and Q77633-46), directed against the consensus
CC   mRNA initiation site sequence (Q77661) for the tenascin gene.  The
CC   polynucleotides are based on the sense strand sequence (Q76387) of the
CC   tenascin gene.  Tenascin is an extracellular matrix glycoprotein
CC   consisting six disulphide-linked subunits, each having molecular mass of
CC   190-250 kDa.  Tenascin may be important for smooth muscle cell
```

```
CC   proliferation as the protein has growth stimulatory activity.  The
CC   polynucleotides can be used to inhibit transcription of the gene or
CC   translation of the mRNA encoding tenascin. The method is applicable to a
CC   number of diseases where the proliferation of smooth muscle is involved
CC   e.g. vascular stenosis, post-angioplasty restenosis and other
CC   non-angioplasty procedures such as cardiac hypertrophy, vascular surgery
CC   and organ transplant.
XX
SQ   Sequence 36 BP; 5 A; 12 C; 8 G; 5 T; 6 other;


  Query Match             100.0%;  Score 14;  DB 15;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 55;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggcccccatggtgg 14
          ||||||||||||||
Db     18 GGCCCCCATGGTGG 5


RESULT  10
Q76386
ID   Q76386 standard; DNA; 36 BP.
XX
AC   Q76386;
XX
DT   01-JUN-1995  (first entry)
XX
DE   Tenascin gene consensus DNA sequence antisense strand.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1..36
FT                   /*tag=  a
FT                   /note= "phosphodiester bonds between nucleotides
FT                          may be replaced by phosphorothioate bonds"
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Claim 1; Page 38; 64pp; English.
XX
CC   A series of antisense polynucleotides, either DNA (Q76388 and Q77619-32)
CC   or RNA (Q76390 and Q77647-60) directed against the sense strand of the
CC   gene encoding tenascin.  The polynucleotides are based on the
CC   complementary sequence (Q76386) of the consensus mRNA initiation site
CC   sequence (Q77661) for the tenascin gene.  Tenascin is an extracellular
CC   matrix glycoprotein consisting six disulphide-linked subunits, each
CC   having molecular mass of 190-250 kDa.  Tenascin may be important for
CC   smooth muscle cell proliferation as the protein has growth stimulatory
CC   activity.  The polynucleotides can be used to inhibit transcription
CC   of the gene or translation of the mRNA encoding tenascin.  The method is
CC   applicable to a number of diseases where the proliferation of smooth
CC   muscle is involved e.g. vascular stenosis, post-angioplasty restenosis
CC   and other non-angioplasty procedures such as cardiac hypertrophy,
CC   vascular surgery and organ transplant.
XX
SQ   Sequence 36 BP; 5 A; 8 C; 12 G; 5 T; 6 other;


  Query Match             100.0%;  Score 14;  DB 15;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 55;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggcccccatggtgg 14
          ||||||||||||||
Db     19 ggcccccatggtgg 32


RESULT  11
Q77661/c
ID   Q77661 standard; RNA; 36 BP.
XX
AC   Q77661;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Tenascin gene mRNA initiation site consensus sequence.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Disclosure; Page 7; 64pp; English.
XX
CC   The  consensus sequence surrounding the initiation site of the mRNA for
CC   the tenascin gene.  The sequence was used to generate the corresponding
CC   DNA sequence (Q77662).  The sequences were the basis for generating a
CC   series of polynucleotides (Q76388-400 and Q77614-60) which were targeted
CC   against either the mRNA or the strand coding for the mRNA of the tenascin
CC   gene.  The polynucleotides can be used to inhibit transcription of the
CC   gene or translation of the mRNA encoding tenascin. Tenascin is an
CC   extracellular matrix glycoprotein consisting six disulphide-linked
CC   subunits, each having molecular mass of 190-250 kDa.  Tenascin may be
CC   important for smooth muscle cell proliferation as the protein has growth
CC   stimulatory activity.  The method is applicable to a number of diseases
CC   where the proliferation of smooth muscle is involved e.g. vascular
CC   stenosis, post-angioplasty restenosis and other non-angioplasty
CC   procedures such as cardiac hypertrophy, vascular surgery and organ
CC   transplant.
XX
SQ   Sequence 36 BP; 5 A; 12 C; 8 G; 5 U; 6 other;
```

```
  Query Match             100.0%;  Score 14;  DB 15;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 55;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ggccccccatggtgg 14
           ||||||||||||||
Db      18 GGCCCCCATGGTGG 5


RESULT  12
Q77662
ID   Q77662 standard; DNA; 36 BP.
XX
AC   Q77662;
XX
DT   02-JUN-1995  (first entry)
XX
DE   Tenascin gene mRNA initiation site complementary DNA sequence.
XX
KW   Antisense; polynucleotide; sense strand; tenascin; complementary;
KW   consensus; initiation; extracellular; glycoprotein; muscle; translation;
KW   proliferation; growth stimulatory; transcription; vascular stenosis;
KW   post-angioplasty; restenosis; cardiac hypertrophy; vascular surgery;
KW   organ transplant; ds.
XX
OS   Synthetic.
XX
PN   WO9421664-A.
XX
PD   29-SEP-1994.
XX
PF   24-MAR-1994;   94WO-US03206.
XX
PR   25-MAR-1993;   93US-0037025.
XX
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
PI   Denner LA,  Dixon RAF,  Rege AA,  Stacy DL;
XX
DR   WPI; 1994-316926/39.
XX
PT   Synthetic anti-sense polynucleotide - hybridises to tenascin
PT   gene, useful for inhibiting vascular smooth muscle cell
PT   proliferation.
XX
PS   Disclosure; Page 54; 64pp; English.
XX
CC   The DNA sequence corresponding to the consensus sequence (Q77661)
CC   surrounding the initiation site of the mRNA for the tenascin gene.  The
CC   sequences were the basis for generating a series of polynucleotides
CC   (Q76386-400 and Q77614-60) which were targeted against either the mRNA or
CC   the strand coding for the mRNA of the tenascin gene.  The polynucleotides
CC   can be used to inhibit transcription of the gene or translation of the
CC   mRNA encoding tenascin. Tenascin is an extracellular matrix glycoprotein
CC   consisting six disulphide-linked subunits, each having molecular mass of
CC   190-250 kDa.  Tenascin may be important for smooth muscle cell
CC   proliferation as the protein has growth stimulatory activity.  The method
CC   is applicable to a number of diseases where the proliferation of smooth
CC   muscle is involved e.g. vascular stenosis, post-angioplasty restenosis
CC   and other non-angioplasty procedures such as cardiac hypertrophy,
CC   vascular surgery and organ transplant.
XX
SQ   Sequence 36 BP; 5 A; 8 C; 12 G; 5 T; 6 other;


  Query Match             100.0%;  Score 14;  DB 15;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 55;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ggccccccatggtgg 14
           ||||||||||||||
Db      19 ggccccccatggtgg 32


RESULT  13
Q80830/c
ID   Q80830 standard; DNA; 24 BP.
XX
AC   Q80830;
XX
DT   11-SEP-1995  (first entry)
XX
DE   Lipopolysaccharide binding protein (rLPB) 5' PCR primer.
XX
KW   Lipopolysaccharide binding protein; rLPB; LPS; 5' PCR primer;
KW   gram-negative bacterial infections; treatment; ss.
XX
OS   Synthetic.
XX
PN   WO9500641-A.
XX
PD   05-JAN-1995.
XX
PF   17-JUN-1994;   94WO-US06931.
XX
PR   17-JUN-1993;   93US-0079510.
XX
PA   (XOMA ) XOMA CORP.
XX
PI   Gazzano-santoro H,  Theofan G,  Trown PW;
XX
DR   WPI; 1995-052078/07.
XX
PT   Lipo:polysaccharide binding protein deriv. and hybrid protein
PT   binds to lipo:polysaccharide - lacks CD14-mediated
PT   immuno:stimulatory properties, used to treat Gram-negative
PT   bacterial infections and associated conditions
XX
PS   Example 2; Page 19; 114pp; English.
XX
CC   Q80830 and Q80831 are a pair of primers for the PCR amplification
CC   of Q80826, which encodes R68922 recombinant lipopolysaccharide (LPS)
CC   binding protein rLPB. The protein R68915 derived from R68922 lacks
CC   CD14-mediated immunostimulatory properties, and can therefore be used
CC   to treat gram-negative bacterial infections and associated
CC   conditions.
XX
SQ   Sequence 24 BP; 4 A; 7 C; 8 G; 5 T; 0 other;


  Query Match             92.9%;  Score 13;  DB 16;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ggccccccatggtg 13
           |||||||||||||
Db      21 GGCCCCCATGGTG 9


RESULT  14
V10334/c
ID   V10334 standard; DNA; 24 BP.
XX
AC   V10334;
XX
DT   05-JUN-1998  (first entry)
XX
DE   Human rLBP PCR primer LBP-3.
XX
KW   Lipopolysaccharide binding protein; LBP; hybrid; lipopolysaccharide;
KW   LPS; bactericidal/permeability increasing protein; BPI; therapeutic;
KW   treatment; Gram-negative bacterial infection; endotoxin; shock;
KW   CD14-mediated immunostimulation; CD-14 receptor; PCR primer; ss.
XX
```

```
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US5731415-A.
XX
PD   24-MAR-1998.
XX
PF   17-JUN-1994;   94US-0261660.
XX
PR   17-JUN-1994;   94US-0261660.
PR   17-JUN-1993;   93US-0079510.
XX
PA   (XOMA ) XOMA CORP.
XX
PI   Gazzano-Santoro H,  Theofan G,  Trown PW;
XX
DR   WPI; 1998-216553/19.
XX
PT   Hybrid lipo-poly:saccharide-binding protein(s) - comprise
PT   bactericidal/permeability-increasing sequences, useful for, e.g.
PT   treating bacterial infection(s)
XX
PS   Example 2; Col 10; 67pp; English.
XX
CC   V10334 and V10335 are PCR primers used in the amplification of a human
CC   recombinant lipopolysaccharide binding protein, LBP. This sequence can
CC   be used to produce hybrid proteins with the lipopolysaccharide (LPS)
CC   binding protein, BPI (bactericidal/permeability increasing protein). Such
CC   hybrids may be used for the production of therapeutic compositions useful
CC   for treating Gram-negative bacterial infections, e.g. endotoxin shock.
CC   These proteins bind to and neutralise lipopolysaccharide but lack
CC   CD14-mediated immunostimulatory properties, including the ability to
CC   mediate LPS activity through CD14 receptors.
XX
SQ   Sequence 24 BP; 4 A; 7 C; 8 G; 5 T; 0 other;


  Query Match             92.9%;  Score 13;  DB 19;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ggcccccatggtg 13
          |||||||||||||
Db     21 GGCCCCCATGGTG 9


RESULT  15
Z61427/c
ID   Z61427 standard; DNA; 24 BP.
XX
AC   Z61427;
XX
DT   19-JUN-2000  (first entry)
XX
DE   PCR primer for DNA encoding short extracellular form of human B7-1.
XX
KW   Short form; B7-1; CD80; T-cell costimulator; antigen presenting cell;
KW   CD28; CTLA4; T cell surface receptor; cytokine production;
KW   cell proliferation; T cell; infection; autoimmune disease; inflammation;
KW   quality assurance; cancer; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200008057-A2.
XX
PD   17-FEB-2000.
XX
PF   05-AUG-1999;   99WO-US17906.
XX
PR   07-AUG-1998;   98US-0095663.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Baum PR;
XX
DR   WPI; 2000-205674/18.
XX
PT   Novel B7L-1 polypeptide and nucleotides encoding them useful as T cell
PT   costimulatory molecules for therapeutics against infections, autoimmune
PT   diseases and inflammation -
XX
PS   Example 4; Page 50; 57pp; English.
XX
CC   PCR primers Z61426-28 were used to amplify DNA encoding the short
CC   extracellular form of human B7-1 (CD80). B7-1 is a T-cell
CC   costimulatory molecule that is found on the surface of antigen
CC   presenting cells (APCs). CD28 and CTLA4 are its T cell surface
CC   receptors. B7-1 interacts with CD28 to signal cytokine production,
CC   cell proliferation, and the generation of effector and memory T cells.
CC   Disorders mediated by interaction of B7-1 and its binding partner,
CC   such as infections, autoimmune diseases and inflammation, are treated
CC   by administering B7L-1 to the disordered mammal. B7L-1 polypeptides
CC   are useful to separate cells expressing a protein to which it binds
CC   and to measure the biological activity of LDCAM polypeptides. They can
CC   also be used as reagents for conducting quality assurance studies e.g.,
CC   to monitor shelf life and stability of proteins to which it binds, and
CC   as carriers for delivering agents attached to cells bearing its counter
CC   structure, LDCAM or other cell receptors. They are also useful as a
CC   research tool for studying T-cell signalling and proliferation. They are
CC   employed in in vitro assays for detecting interactions of LDCAM with
CC   T-cell receptors. Diagnostic and therapeutic agents, such as drugs,
CC   toxins, radionuclides, chromophores, and enzymes which catalyse a
CC   colorimetric or fluorometric reaction, may be attached to a B7L-1
CC   polypeptide, e.g. nitrogen mustards are attached to the B7L-1
CC   and used to treat various forms of cancer.
XX
SQ   Sequence 24 BP; 5 A; 7 C; 8 G; 4 T; 0 other;


  Query Match             92.9%;  Score 13;  DB 21;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 gcccccatggtgg 14
          |||||||||||||
Db     24 GCCCCCATGGTGG 12


Search completed: March 23, 2001, 16:04:32
Job time: 35931 sec
```

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 23, 2001, 15:55:10 ; Search time 319.44 Seconds
(without alignments)
7.568 Million cell updates/sec

Title: US-09-554-267-9
Perfect score: 15
Sequence: 1 gcgagggcaaggaaa 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 280836 seqs, 80580151 residues

Total number of hits satisfying chosen parameters: 402106

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	12.4	82.7	26	5	5455029-17	Patent No. 5455029
	2	12	80.0	21	1	US-08-446-530-22	Sequence 22, Appl
	3	12	80.0	21	2	US-09-097-562-22	Sequence 22, Appl
	4	11.8	78.7	45	2	US-08-832-449A-7	Sequence 7, Appli
	5	11.4	76.0	29	2	US-08-960-022-23	Sequence 23, Appl
c	6	11.4	76.0	40	1	US-08-199-507B-33	Sequence 33, Appl
c	7	11.4	76.0	40	1	US-08-441-828-33	Sequence 33, Appl
c	8	11	73.3	30	3	US-08-467-023-196	Sequence 196, App
	9	10.8	72.0	18	1	US-08-525-654A-140	Sequence 140, App
	10	10.8	72.0	19	1	US-08-152-313-39	Sequence 39, Appl
	11	10.8	72.0	19	1	US-08-579-223-39	Sequence 39, Appl
	12	10.8	72.0	19	3	US-08-181-664-26	Sequence 26, Appl
	13	10.8	72.0	19	4	PCT-US94-12947A-39	Sequence 39, Appl
	14	10.8	72.0	24	3	US-08-795-430-36	Sequence 36, Appl
c	15	10.8	72.0	25	2	US-08-557-128-34	Sequence 34, Appl
	16	10.8	72.0	25	3	US-08-852-629-16	Sequence 16, Appl
c	17	10.8	72.0	27	3	US-08-776-246-3	Sequence 3, Appli
c	18	10.8	72.0	27	3	US-08-776-251-7	Sequence 7, Appli
	19	10.8	72.0	30	2	US-08-771-850A-5	Sequence 5, Appli
c	20	10.8	72.0	31	1	US-08-750-007-16	Sequence 16, Appl
c	21	10.8	72.0	32	3	US-09-009-156-14	Sequence 14, Appl
c	22	10.8	72.0	36	1	US-08-413-813-4	Sequence 4, Appli
c	23	10.8	72.0	36	2	US-08-467-346-4	Sequence 4, Appli
	24	10.8	72.0	42	3	US-08-975-703-31	Sequence 31, Appl
	25	10.8	72.0	45	2	US-08-588-201-9	Sequence 9, Appli
	26	10.8	72.0	45	2	US-09-169-605-9	Sequence 9, Appli
	27	10.8	72.0	45	3	US-08-893-327-9	Sequence 9, Appli
	28	10.4	69.3	20	2	US-08-313-185-25	Sequence 25, Appl
c	29	10.4	69.3	20	3	US-09-166-186-85	Sequence 85, Appl
	30	10.4	69.3	20	3	US-09-082-614A-25	Sequence 25, Appl
	31	10.4	69.3	23	2	US-08-859-998-697	Sequence 697, App
	32	10.4	69.3	24	2	US-08-859-998-1177	Sequence 1177, Ap
c	33	10.4	69.3	25	1	US-08-211-430-5	Sequence 5, Appli
	34	10.4	69.3	26	2	US-08-726-090-8	Sequence 8, Appli
c	35	10.4	69.3	30	1	US-08-802-547-1	Sequence 1, Appli
	36	10.4	69.3	30	1	US-08-802-547-5	Sequence 5, Appli
c	37	10.4	69.3	30	1	US-08-712-357-1	Sequence 1, Appli
	38	10.4	69.3	30	1	US-08-712-357-5	Sequence 5, Appli
c	39	10.4	69.3	30	3	US-08-801-154-7	Sequence 7, Appli
c	40	10.4	69.3	30	3	US-08-873-709-16	Sequence 16, Appl
	41	10.4	69.3	33	3	US-08-801-154-3	Sequence 3, Appli
	42	10.4	69.3	33	3	US-08-873-709-12	Sequence 12, Appl
c	43	10.4	69.3	36	1	US-07-988-194A-27	Sequence 27, Appl
c	44	10.4	69.3	36	1	US-08-258-152-29	Sequence 29, Appl
c	45	10.4	69.3	36	2	US-08-076-299A-29	Sequence 29, Appl

ALIGNMENTS

```
RESULT   1
5455029-17
;Patent No. 5455029
;    APPLICANT: HARTMAN, JACOB R.;OPPENHEIM, AMOS B.;GORECKI,
;MARIAN;AVIV, HAIM;OREN, RACHEL
;    TITLE OF INVENTION: THERAPEUTIC COMPOSITIONS COMPRISING
;A MIXTURE OF HUMAN CUZN SUPEROXIDE DISMUTASE ANALOGS
;    NUMBER OF SEQUENCES: 30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/933,500
;      FILING DATE: 21-AUG-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 449,125
;      FILING DATE: 08-DEC-1989
;      APPLICATION NUMBER: 202,238
;      FILING DATE: 03JUN-1988
;      APPLICATION NUMBER: 897,056
;      FILING DATE: 14-AUG-1985
;      APPLICATION NUMBER: 767,143
;      FILING DATE: 19-AUG-1985
;      APPLICATION NUMBER: 644,245
;      FILING DATE: 27-AUG-1984
;SEQ ID NO:17:
;      LENGTH: 26
5455029-17


  Query Match             82.7%;  Score 12.4;  DB 5;  Length 26;
  Best Local Similarity   92.9%;  Pred. No. 3.2e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 cgagggcaaggaaa 15
           |||| |||||||||
Db       5 cgagcgcaaggaaa 18


RESULT   2
US-08-446-530-22
; Sequence 22, Application US/08446530
; Patent No. 5766851
;  GENERAL INFORMATION:
;    APPLICANT:  Shuldiner, Alan R.
;    APPLICANT:  Walston, Jeremy
;    APPLICANT:  Silver, Kristi
;    TITLE OF INVENTION:  SUSCEPTIBILITY GENE FOR OBESITY AND TYPE
;    TITLE OF INVENTION:  II DIABETES MELLITUS
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square
;      CITY:  La Jolla
```

```
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,530
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haile, Lisa A.
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  07265/048001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5070
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-446-530-22


  Query Match             80.0%;  Score 12;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.1e+02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 agggcaaggaaa 15
          ||||||||||||
Db      2 AGGGCAAGGAAA 13


RESULT   3
US-09-097-562-22
; Sequence 22, Application US/09097562
; Patent No. 5877283
;  GENERAL INFORMATION:
;    APPLICANT:  Shuldiner, Alan R.
;    APPLICANT:  Walston, Jeremy
;    APPLICANT:  Silver, Kristi
;    TITLE OF INVENTION:  SUSCEPTIBILITY GENE FOR OBESITY AND TYPE
;    TITLE OF INVENTION:  II DIABETES MELLITUS
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/097,562
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/446,530
;      FILING DATE:  19-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haile, Lisa A.
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  07265/048001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5070
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-097-562-22


  Query Match             80.0%;  Score 12;  DB 2;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.1e+02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 agggcaaggaaa 15
          ||||||||||||
Db      2 AGGGCAAGGAAA 13


RESULT   4
US-08-832-449A-7
; Sequence 7, Application US/08832449A
; Patent No. 5849497
;  GENERAL INFORMATION:
;    APPLICANT:  CHARLES STEINMAN
;    TITLE OF INVENTION:  SPECIFIC INHIBITION OF THE
;    TITLE OF INVENTION:  POLYMERASE CHAIN REACTION USING
;    TITLE OF INVENTION:  A NON-EXTENDABLE OLIGONUCLEOTIDE
;    TITLE OF INVENTION:  BLOCKER
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Meltzer, Lippe, Goldstein,
;      ADDRESSEE:  Wolf & Schlissel, P.C.
;      STREET:  190 Willis Avenue
;      CITY:  Mineola
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  11501
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 800 Kb storage
;      COMPUTER:  PC Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  WordPerfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/832,449A
;      FILING DATE:  03-April-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  GUTTMAN, CHARLES
;      REGISTRATION NUMBER:  29,161
;      REFERENCE/DOCKET NUMBER:  4421-4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 747-0300
;      TELEFAX:  (516) 747-5638
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  45 base pairs
;      TYPE:  Nucleic Acids
;      STRANDEDNESS:  Single Stranded
;      TOPOLOGY:  Linear
;    MOLECULE TYPE:  Genomic DNA
US-08-832-449A-7


  Query Match             78.7%;  Score 11.8;  DB 2;  Length 45;
  Best Local Similarity   86.7%;  Pred. No. 6.7e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 gcgagggcaaggaaa 15
          |||||| |||| |||
Db     24 GCGAGGTCAAGCAAA 38
```